

WEST Search History

[Hide Items] [Restore] [Clear] [Cancel]

DATE: Saturday, September 24, 2005

Hide? Set Name Query

Hit Count

DB=USPT; PLUR=YES; OP=OR

<input type="checkbox"/>	L1	6294662.pn.	1
<input type="checkbox"/>	L2	6683156.pn.	1
<input type="checkbox"/>	L3	6649588.pn. or 6428966.pn. or 6294662.pn. or 5916751.pn.	4
<input type="checkbox"/>	L4	Tabibzadeh.in.	7

END OF SEARCH HISTORY

WEST Search History

[Hide Items](#) [Restore](#) [Clear](#) [Cancel](#)

DATE: Saturday, September 24, 2005

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
<i>DB=USPT; PLUR=YES; OP=OR</i>			
<input type="checkbox"/>	L1	5874479.pn.	1
<input type="checkbox"/>	L2	tgf\$ same (type4 or type-4 or (type near 4))	15
<input type="checkbox"/>	L3	(lefty1 or lefty2 or lefty-1 or lefty-2 or leftyb or lefty-b or leftya or lefty-a) and protein	6
<input type="checkbox"/>	L4	(stra3 or stra-3) and protein	13
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR</i>			
<input type="checkbox"/>	L5	(lefty1 or lefty2 or lefty-1 or lefty-2 or leftyb or lefty-b or leftya or lefty-a) and protein	18
<input type="checkbox"/>	L6	L5 not l3	12
<input type="checkbox"/>	L7	L5 not l3	12
<input type="checkbox"/>	L8	(stra3 or stra-3) and protein	96
<input type="checkbox"/>	L9	(stra3 or stra-3) same (protein or polypeptide or peptide)	95
<input type="checkbox"/>	L10	transforming near growth near factor near beta near 4	74
<input type="checkbox"/>	L11	L10 not l2	74
<input type="checkbox"/>	L12	L11 not l3	74
<input type="checkbox"/>	L13	L12 not l5	74

END OF SEARCH HISTORY

Trying 31060000009999...Open

DIALOG INFORMATION SERVICES

PLEASE LOGON:

***** HHHHHHHH SSSSSSS? ### Status: Signing onto Dialog *****
ENTER PASSWORD:

***** HHHHHHHH SSSSSSS? *****

Status: Login successfulWelcome to DIALOG

Dialog level 05.06.01D

Last logoff: 21sep05 09:05:16

Logon file405 26sep05 07:14:32

*** ANNOUNCEMENT ***

--UPDATED: Important Notice to Freelance Authors--

See HELP FREELANCE for more information

NEW FILES RELEASED

***Computer and Information Systems Abstracts (File 56)
***Electronics and Communications Abstracts (File 57)
***Solid State and Superconductivity Abstracts (File 68)
***ANTE: Abstracts in New Technologies (File 60)
***Civil Engineering Abstracts (File 61)
***Aluminium Industry Abstracts (File 33)
***Ceramic Abstracts/World Ceramic Abstracts (File 335)
***CSA Life Sciences Abstracts (File 24)
***Corrosion Abstracts (File 46)
***Materials Business File (File 269)
***Engineered Materials Abstracts (File 293)
***CSA Aerospace & High Technology Database (File 108)
***CSA Technology Research Database (File 23)
***METADEX(r) (File 32)
***FDAnews (File 182)
***German Patents Fulltext (File 324)

RESUMED UPDATING

***Canadian Business and Current Affairs (262)
***CorpTech (559)

Chemical Structure Searching now available in Prous Science Drugs
of the Future (F453), IMS R&D Focus (F445), Beilstein Facts (F390),
and Derwent Chemistry Resource (F355).

>>> Enter BEGIN HOMEBASE for Dialog Announcements <<
>>> of new databases, price changes, etc. <<

* * *

SYSTEM:HOME

Cost is in DialUnits

Menu System II: D2 version 1.7.9 term=ASCII

*** DIALOG HOMEBASE(SM) Main Menu ***

Information:

1. Announcements (new files, reloads, etc.)
2. Database, Rates, & Command Descriptions
3. Help in Choosing Databases for Your Topic
4. Customer Services (telephone assistance, training, seminars, etc.)
5. Product Descriptions

Connections:

- 6. DIALOG(R) Document Delivery
- 7. Data Star(R)

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/H = Help

/L = Logoff

/NOMENU = Command Mode

Enter an option number to view information or to connect to an online service. Enter a BEGIN command plus a file number to search a database (e.g., B1 for ERIC).

? b 155 medicine

Terminal set to DLINK

*** DIALOG HOMEBASE(SM) Main Menu ***

Information:

- 1. Announcements (new files, reloads, etc.)
- 2. Database, Rates, & Command Descriptions
- 3. Help in Choosing Databases for Your Topic
- 4. Customer Services (telephone assistance, training, seminars, etc.)
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Connections:

- 6. DIALOG(R) Document Delivery
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/H = Help

/L = Logoff

/NOMENU = Command Mode

Enter an option number to view information or to connect to an online service. Enter a BEGIN command plus a file number to search a database (e.g., B1 for ERIC).

? e transforming growth factor beta

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26sep05 07:14:34 User228206 Session D2511.1
$0.00 0.211 DialUnits FileHomeBase
$0.00 Estimated cost FileHomeBase
$0.00 Estimated cost this search
$0.00 Estimated total session cost 0.211 DialUnits
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SYSTEM:OS - DIALOG OneSearch

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File 155:MEDLINE(R) 1951-2005/Sep 26
      (c) format only 2005 Dialog
File 5:Biosis Previews(R) 1969-2005/Sep W3
      (c) 2005 BIOSIS
File 34:SciSearch(R) Cited Ref Sci 1990-2005/Sep W3
      (c) 2005 Inst for Sci Info
File 35:Dissertation Abs Online 1861-2005/Aug
      (c) 2005 ProQuest Info&Learning
File 48:SPORTDiscus 1962-2005/Apr
      (c) 2005 Sport Information Resource Centre
File 65:Inside Conferences 1993-2005/Sep W3
      (c) 2005 BLDSC all rts. reserv.
File 71:ELSEVIER BIOBASE 1994-2005/Sep W3
      (c) 2005 Elsevier Science B.V.
File 73:EMBASE 1974-2005/Sep 26
      (c) 2005 Elsevier Science B.V.
File 91:MANTIS(TM) 1880-2005/Jun
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2001 (c) Action Potential
 File 94:JICST-EPlus 1985-2005/Jul W5
 (c) 2005 Japan Science and Tech Corp (JST)
 File 98:General Sci Abs/Full-Text 1984-2004/Dec
 (c) 2005 The HW Wilson Co.
 File 135:NewsRx Weekly Reports 1995-2005/Sep W3
 (c) 2005 NewsRx

*File 135: New newsletters are now added. See Help News135 for the complete list of newsletters.

File 144:Pascal 1973-2005/Sep W3
 (c) 2005 INIST/CNRS
 File 149:TGG Health&Wellness DB(SM) 1976-2005/Sep W3
 (c) 2005 The Gale Group
 File 156:ToxFile 1965-2005/Sep W4
 (c) format only 2005 Dialog
 File 159:Cancerlit 1975-2002/Oct
 (c) format only 2002 Dialog

*File 159: Cancerlit is no longer updating.

Please see HELP NEWS159.

File 162:Global Health 1983-2005/Aug
 (c) 2005 CAB International
 File 164:Allied & Complementary Medicine 1984-2005/Sep
 (c) 2005 BLHCIS
 File 172:EMBASE Alert 2005/Sep 26
 (c) 2005 Elsevier Science B.V.
 File 266:FEDRIP 2005/Jun
 Comp & dist by NTIS, Int'l Copyright All Rights Res
 File 369:New Scientist 1994-2005/Jun W4
 (c) 2005 Reed Business Information Ltd.
 File 370:Science 1996-1999/Jul W3
 (c) 1999 AAAS

*File 370: This file is closed (no updates). Use File 47 for more current information.

File 399:CA SEARCH(R) 1967-2005/UD=14313
 (c) 2005 American Chemical Society

*File 399: Use is subject to the terms of your user/customer agreement.
 Alert feature enhanced for multiple files, etc. See HELP ALERT.

File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
 (c) 1998 Inst for Sci Info
 File 444:New England Journal of Med. 1985-2005/Sep W2
 (c) 2005 Mass. Med. Soc.
 File 467:ExtraMED(tm) 2000/Dec
 (c) 2001 Informania Ltd.

*File 467: F467 no longer updates; see Help News467.

7.

Set	Items	Description
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Ref	Items	RT Index-term
E1	2	TRANSFORMING GROWTH FACTOR B-1
E2	1	TRANSFORMING GROWTH FACTOR B-1 TGF-B1
E3	62977	39 *TRANSFORMING GROWTH FACTOR BETA
E4	1	TRANSFORMING GROWTH FACTOR BETA (TGF-BETA)
E5	1	TRANSFORMING GROWTH FACTOR BETA (TAFB)
E6	7	TRANSFORMING GROWTH FACTOR BETA (TGF BETA)
E7	1	TRANSFORMING GROWTH FACTOR BETA (TGF)-BETA(1)
E8	1	TRANSFORMING GROWTH FACTOR BETA (TGF- BETA)
E9	47	TRANSFORMING GROWTH FACTOR BETA (TGF-BETA)
E10	1	TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) AND REC
E11	2	TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) REC

E12 4 TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) SUP

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Ref	Items	Type	RT	Index-term
R1	57199		39	*TRANSFORMING GROWTH FACTOR BETA
R2	3518	U	2	TGF BETA
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R4	14733	X		DC=D11.303.900.720.
R5	25165	X		DC=D12.644.276.984.720.
R6	14733	X		DC=D12.644.900.720.
R7	39898	X		DC=D24.185.348.900.720.
R8	278463			DC=D24.35.190
R9	130149			DC=D24.35.540.360
R10	39898	X		DC=D24.611.350.400.800.
R11	0	X	3	BONE-DERIVED TRANSFORMING GROWTH FACTOR
R12	0	X	3	PLATELET TRANSFORMING GROWTH FACTOR

Enter P or PAGE for more

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Ref	Items	Type	RT	Index-term
R13	8	X	3	TGF-BETA
R14	43232	B	352	GROWTH SUBSTANCES
R15	3919	B	21	TRANSFORMING GROWTH FACTORS
R16	130149			DC=D29.25.540.360
R17	278463			DC=D4.680.190
R18	130149			DC=D4.680.360
R19	120579	B	266	CYTOKINE
R20	19791	B	153	GROWTH FACTOR
R21	0	S	1	BETA TRANSFORMING GROWTH FACTOR
R22	0	S	1	PLATELET DERIVED TRANSFORMING GROWTH FACTOR BE
R23	0	S	1	TRANSFORMING GROWTH FACTOR TYPE BETA
R24	0	S	1	TYPE BETA TRANSFORMING GROWTH FACTOR

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>>>Related terms display completed...

? e transforming growth factor b

Ref	Items	RT	Index-term
E1	1		TRANSFORMING GROWTH FACTOR ANTISENSE MESSENGER
E2	1		TRANSFORMING GROWTH FACTOR AUTOCRINE GROWTH FA
E3	12		*TRANSFORMING GROWTH FACTOR B
E4	1		TRANSFORMING GROWTH FACTOR B (TGF-BETA) SOLUBL
E5	1		TRANSFORMING GROWTH FACTOR B IODODEOXYURIDINE
E6	1		TRANSFORMING GROWTH FACTOR B- SUPERFAMILY
E7	1		TRANSFORMING GROWTH FACTOR B-BETA
E8	2		TRANSFORMING GROWTH FACTOR B-1
E9	1		TRANSFORMING GROWTH FACTOR B-1 TGF-B1
E10	62977	39	TRANSFORMING GROWTH FACTOR BETA
E11	1		TRANSFORMING GROWTH FACTOR BETA (TGF-BETA)
E12	1		TRANSFORMING GROWTH FACTOR BETA (TAFB)

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Ref	Items	Index-term
E13	7	TRANSFORMING GROWTH FACTOR BETA (TGF BETA)
E14	1	TRANSFORMING GROWTH FACTOR BETA (TGF)-BETA(1)
E15	1	TRANSFORMING GROWTH FACTOR BETA (TGF- BETA)

E16 47 TRANSFORMING GROWTH FACTOR BETA (TGF-BETA)
E17 1 TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) AND
E18 2 TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) REC
E19 4 TRANSFORMING GROWTH FACTOR BETA (TGF-BETA) SUP
E20 1 TRANSFORMING GROWTH FACTOR BETA (TGF-P) AND PR
E21 1 TRANSFORMING GROWTH FACTOR BETA (TGF-P) SOLUBL
E22 5 TRANSFORMING GROWTH FACTOR BETA (TGF^BETA)
E23 1 TRANSFORMING GROWTH FACTOR BETA (TGF^BETA1)
E24 612 TRANSFORMING GROWTH FACTOR BETA --ADMINISTRATI

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E25 8 TRANSFORMING GROWTH FACTOR BETA --ADVERSE DRUG
E26 66 TRANSFORMING GROWTH FACTOR BETA --ADVERSE EFFE
E27 21 TRANSFORMING GROWTH FACTOR BETA --AGONISTS --A
E28 2318 TRANSFORMING GROWTH FACTOR BETA --ANALYSIS --A
E29 1290 TRANSFORMING GROWTH FACTOR BETA --ANTAGONISTS
E30 4167 TRANSFORMING GROWTH FACTOR BETA --BIOSYNTHESIS
E31 1298 TRANSFORMING GROWTH FACTOR BETA --BLOOD --BL
E32 3 TRANSFORMING GROWTH FACTOR BETA --BUCCAL DRUG
E33 80 TRANSFORMING GROWTH FACTOR BETA --CEREBROSPINA
E34 2 TRANSFORMING GROWTH FACTOR BETA --CHEMICAL SYN
E35 569 TRANSFORMING GROWTH FACTOR BETA --CHEMISTRY --
E36 92 TRANSFORMING GROWTH FACTOR BETA --CLASSIFICATI

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E37 23 TRANSFORMING GROWTH FACTOR BETA --CLINICAL TRI
E38 144 TRANSFORMING GROWTH FACTOR BETA --DEFICIENCY --
E39 9 TRANSFORMING GROWTH FACTOR BETA --DIAGNOSTIC U
E40 15 TRANSFORMING GROWTH FACTOR BETA --DRUG ADMINIS
E41 22 TRANSFORMING GROWTH FACTOR BETA --DRUG ANALYSI
E42 198 TRANSFORMING GROWTH FACTOR BETA --DRUG COMBINA
E43 237 TRANSFORMING GROWTH FACTOR BETA --DRUG COMPARI
E44 13 TRANSFORMING GROWTH FACTOR BETA --DRUG CONCENT
E45 102 TRANSFORMING GROWTH FACTOR BETA --DRUG DEVELOP
E46 175 TRANSFORMING GROWTH FACTOR BETA --DRUG DOSE --
E47 402 TRANSFORMING GROWTH FACTOR BETA --DRUG EFFECTS
E48 105 TRANSFORMING GROWTH FACTOR BETA --DRUG INTERAC

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E49 272 TRANSFORMING GROWTH FACTOR BETA --DRUG THERAPY
E50 25 TRANSFORMING GROWTH FACTOR BETA --DRUG TOXICIT
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E1 25 TRANSFORMING GROWTH FACTOR BETA --DRUG TOXICIT
E2 9023 TRANSFORMING GROWTH FACTOR BETA --ENDOGENOUS C
E3 8384 TRANSFORMING GROWTH FACTOR BETA --GENETICS --G
E4 2 TRANSFORMING GROWTH FACTOR BETA --HISTORY --HI
E5 1771 TRANSFORMING GROWTH FACTOR BETA --IMMUNOLOGY --
E6 1 TRANSFORMING GROWTH FACTOR BETA --INTRAARTERIA
E7 5 TRANSFORMING GROWTH FACTOR BETA --INTRAARTICUL
E8 1 TRANSFORMING GROWTH FACTOR BETA --INTRACARDIAC

E9 1 TRANSFORMING GROWTH FACTOR BETA --INTRACAVERNO
E10 4 TRANSFORMING GROWTH FACTOR BETA --INTRACEREBRA
E11 1 TRANSFORMING GROWTH FACTOR BETA --INTRACEREBRO
E12 1 TRANSFORMING GROWTH FACTOR BETA --INTRACISTERN

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E13 1 TRANSFORMING GROWTH FACTOR BETA --INTRADERMAL
E14 1 TRANSFORMING GROWTH FACTOR BETA --INTRAGASTRIC
E15 6 TRANSFORMING GROWTH FACTOR BETA --INTRAMUSCULA
E16 5 TRANSFORMING GROWTH FACTOR BETA --INTRANASAL D
E17 1 TRANSFORMING GROWTH FACTOR BETA --INTRAOCULAR
E18 4 TRANSFORMING GROWTH FACTOR BETA --INTRAPERITON
E19 2 TRANSFORMING GROWTH FACTOR BETA --INTRAPLEURAL
E20 5 TRANSFORMING GROWTH FACTOR BETA --INTRAVENOUS
E21 197 TRANSFORMING GROWTH FACTOR BETA --ISOLATION AN
E22 9153 TRANSFORMING GROWTH FACTOR BETA --METABOLISM -
E23 4 TRANSFORMING GROWTH FACTOR BETA --ORAL DRUG AD
E24 1 TRANSFORMING GROWTH FACTOR BETA --PARENTERAL D

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E25 75 TRANSFORMING GROWTH FACTOR BETA --PHARMACEUTIC
E26 3 TRANSFORMING GROWTH FACTOR BETA --PHARMAOECON
E27 62 TRANSFORMING GROWTH FACTOR BETA --PHARMACOKINE
E28 14529 TRANSFORMING GROWTH FACTOR BETA --PHARMACOLOGY
E29 6647 TRANSFORMING GROWTH FACTOR BETA --PHYSIOLOGY -
E30 63 TRANSFORMING GROWTH FACTOR BETA --RADIATION EF
E31 678 TRANSFORMING GROWTH FACTOR BETA --SECRETION --
E32 4 TRANSFORMING GROWTH FACTOR BETA --STANDARDS --
E33 4 TRANSFORMING GROWTH FACTOR BETA --SUBCUTANEOUS
E34 597 TRANSFORMING GROWTH FACTOR BETA --THERAPEUTIC
E35 13 TRANSFORMING GROWTH FACTOR BETA --TOPICAL DRUG
E36 102 TRANSFORMING GROWTH FACTOR BETA --TOXICITY --T

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Ref Items RT Index-term
E37 131 TRANSFORMING GROWTH FACTOR BETA --URINE --UR
E38 4517 TRANSFORMING GROWTH FACTOR BETA //RECEPTORS,
E39 1 TRANSFORMING GROWTH FACTOR BETA ACTIVATED
E40 1 TRANSFORMING GROWTH FACTOR BETA ACTIVATED BIND
E41 62 6 TRANSFORMING GROWTH FACTOR BETA ACTIVATED KINA
E42 2 TRANSFORMING GROWTH FACTOR BETA ACTIVATED PROT
E43 1 TRANSFORMING GROWTH FACTOR BETA ACTIVATING KIN
E44 1 TRANSFORMING GROWTH FACTOR BETA ACTIVATION
E45 1 TRANSFORMING GROWTH FACTOR BETA ACTIVATOR PROT
E46 1 TRANSFORMING GROWTH FACTOR BETA ACTIVIN RECEP
E47 1 TRANSFORMING GROWTH FACTOR BETA ACTIVIN RESPON
E48 1 TRANSFORMING GROWTH FACTOR BETA ACTIVITY

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E49 1 TRANSFORMING GROWTH FACTOR BETA ALPHA

E50 10 TRANSFORMING GROWTH FACTOR BETA ANTAGONIST

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Ref	Items	RT	Index-term
E1	10		TRANSFORMING GROWTH FACTOR BETA ANTAGONIST
E2	196	8	TRANSFORMING GROWTH FACTOR BETA ANTIBODY
E3	3		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --ADV
E4	6		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --CLI
E5	56		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --DRU
E6	4		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --END
E7	12		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --INT
E8	59		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --PHA
E9	3		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --SUB
E10	1		TRANSFORMING GROWTH FACTOR BETA ANTIBODY --TOP
E11	1		TRANSFORMING GROWTH FACTOR BETA ASSOCIATED KIN
E12	1		TRANSFORMING GROWTH FACTOR BETA ASSOCIATED PEP

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Ref	Items	Index-term
E13	7	TRANSFORMING GROWTH FACTOR BETA BINDING PROTEI
E14	1	TRANSFORMING GROWTH FACTOR BETA CARTILAGE REGU
E15	1	TRANSFORMING GROWTH FACTOR BETA CDNA
E16	1	TRANSFORMING GROWTH FACTOR BETA COMPLEMENTARY
E17	2	TRANSFORMING GROWTH FACTOR BETA CONTROL ELEMEN
E18	2	TRANSFORMING GROWTH FACTOR BETA DERIVATIVE
E19	1	TRANSFORMING GROWTH FACTOR BETA EPIDERMAL GROW
E20	2	TRANSFORMING GROWTH FACTOR BETA FAMILY
E21	3	TRANSFORMING GROWTH FACTOR BETA FAMILY MEMBER
E22	2	TRANSFORMING GROWTH FACTOR BETA FAMILY MEMBERS
E23	1	TRANSFORMING GROWTH FACTOR BETA FAMILY OF SECR
E24	1	TRANSFORMING GROWTH FACTOR BETA FSH IMMUNOREAC

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Ref	Items	Index-term
E25	2	TRANSFORMING GROWTH FACTOR BETA GENE
E26	2	TRANSFORMING GROWTH FACTOR BETA GENES
E27	1	TRANSFORMING GROWTH FACTOR BETA GROWTH FACTOR
E28	1	TRANSFORMING GROWTH FACTOR BETA I RECEPTOR
E29	1	TRANSFORMING GROWTH FACTOR BETA I TGFBI
E30	11	TRANSFORMING GROWTH FACTOR BETA I 125
E31	2	TRANSFORMING GROWTH FACTOR BETA I-ASSOCIATED P
E32	1	TRANSFORMING GROWTH FACTOR BETA II
E33	5	TRANSFORMING GROWTH FACTOR BETA II RECEPTOR
E34	1	TRANSFORMING GROWTH FACTOR BETA II RECEPTOR IM
E35	2	TRANSFORMING GROWTH FACTOR BETA IMMUNOGLOBULIN
E36	1	TRANSFORMING GROWTH FACTOR BETA IMMUNOHISTOCHE

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Ref	Items	Index-term
E37	1	TRANSFORMING GROWTH FACTOR BETA IMMUNOSUPPRESS
E38	1	TRANSFORMING GROWTH FACTOR BETA INDUCED FACTOR
E39	3	TRANSFORMING GROWTH FACTOR BETA INDUCED GENE
E40	1	TRANSFORMING GROWTH FACTOR BETA INDUCED GENE H
E41	4	TRANSFORMING GROWTH FACTOR BETA INDUCIBLE EARL
E42	5	TRANSFORMING GROWTH FACTOR BETA INDUCIBLE GENE

E43 1 TRANSFORMING GROWTH FACTOR BETA INDUCIBLE IMME
E44 1 TRANSFORMING GROWTH FACTOR BETA INDUCIBLE PROT
E45 1 TRANSFORMING GROWTH FACTOR BETA INHIBITED MEMB
E46 4 TRANSFORMING GROWTH FACTOR BETA INHIBITOR
E47 1 TRANSFORMING GROWTH FACTOR BETA INHIBITORY ELE
E48 1 TRANSFORMING GROWTH FACTOR BETA ISOFORM

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Ref Items Index-term
E49 1 TRANSFORMING GROWTH FACTOR BETA ISOFORM OVEREX
E50 3 TRANSFORMING GROWTH FACTOR BETA ISOFORMS
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S1 3 'TRANSFORMING GROWTH FACTOR BETA ISOFORMS'

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Ref Items RT Index-term
E1 3 TRANSFORMING GROWTH FACTOR BETA ISOFORMS
E2 1 TRANSFORMING GROWTH FACTOR BETA L
E3 1 1 TRANSFORMING GROWTH FACTOR BETA LATENCY ASSOCI
E4 1 TRANSFORMING GROWTH FACTOR BETA LATENCY BINDIN
E5 1 TRANSFORMING GROWTH FACTOR BETA LIKE BINDING P
E6 9 TRANSFORMING GROWTH FACTOR BETA MASKING PROTEI
E7 1 TRANSFORMING GROWTH FACTOR BETA MEMBER
E8 4 TRANSFORMING GROWTH FACTOR BETA MESSENGER RNA
E9 1 TRANSFORMING GROWTH FACTOR BETA MONOCLONAL ANT
E10 1 TRANSFORMING GROWTH FACTOR BETA MONONUCLEAR MA
E11 1 TRANSFORMING GROWTH FACTOR BETA MRNA TGF-BETA
E12 3 TRANSFORMING GROWTH FACTOR BETA MRNA TRANSFORM

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Ref Items Index-term
E13 3 TRANSFORMING GROWTH FACTOR BETA NEUTRALIZING A
E14 1 TRANSFORMING GROWTH FACTOR BETA ONE
E15 1 TRANSFORMING GROWTH FACTOR BETA ONE (TGF-BETA)
E16 1 TRANSFORMING GROWTH FACTOR BETA OSTEOCALCIN CO
E17 1 TRANSFORMING GROWTH FACTOR BETA PALATE MORPHOG
E18 1 TRANSFORMING GROWTH FACTOR BETA PATHWAY
E19 1 TRANSFORMING GROWTH FACTOR BETA PDGFR
E20 1 TRANSFORMING GROWTH FACTOR BETA PLATELET DERIV
E21 1 TRANSFORMING GROWTH FACTOR BETA PLATELET FACTO
E22 1 TRANSFORMING GROWTH FACTOR BETA PLATELET-DERIV
E23 1 TRANSFORMING GROWTH FACTOR BETA POLYPEPTIDE
E24 61 TRANSFORMING GROWTH FACTOR BETA PRECURSOR

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Ref Items RT Index-term
E25 2 TRANSFORMING GROWTH FACTOR BETA PROTEIN
E26 1 TRANSFORMING GROWTH FACTOR BETA PSEUDORECEPTOR
E27 2287 7 TRANSFORMING GROWTH FACTOR BETA RECEPTOR
E28 1 TRANSFORMING GROWTH FACTOR BETA RECEPTOR --ADV
E29 2 TRANSFORMING GROWTH FACTOR BETA RECEPTOR --CLI
E30 53 TRANSFORMING GROWTH FACTOR BETA RECEPTOR --DRU
E31 1439 TRANSFORMING GROWTH FACTOR BETA RECEPTOR --END
E32 13 TRANSFORMING GROWTH FACTOR BETA RECEPTOR --INT
E33 45 TRANSFORMING GROWTH FACTOR BETA RECEPTOR --PHA

E34 1 TRANSFORMING GROWTH FACTOR BETA RECEPTOR --SUB
E35 2 TRANSFORMING GROWTH FACTOR BETA RECEPTOR --TOP
E36 1 TRANSFORMING GROWTH FACTOR BETA RECEPTOR AGONI

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Ref	Items	RT	Index-term
E37	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ALK1
E38	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ALK2
E39	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ALK5
E40	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ALK8
E41	7		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ANTAG
E42	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR ASSOC
E43	2		TRANSFORMING GROWTH FACTOR BETA RECEPTOR BLOCK
E44	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR EXPRE
E45	6		TRANSFORMING GROWTH FACTOR BETA RECEPTOR FAMIL
E46	20		TRANSFORMING GROWTH FACTOR BETA RECEPTOR I
E47	3		TRANSFORMING GROWTH FACTOR BETA RECEPTOR I KIN
E48	34	1	TRANSFORMING GROWTH FACTOR BETA RECEPTOR II

Enter P or PAGE for more

? p

Ref	Items	Index-term
E49	1	TRANSFORMING GROWTH FACTOR BETA RECEPTOR II GE
E50	1	TRANSFORMING GROWTH FACTOR BETA RECEPTOR II TG

? p

Ref	Items	RT	Index-term
E1	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR II TG
E2	8		TRANSFORMING GROWTH FACTOR BETA RECEPTOR III
E3	2		TRANSFORMING GROWTH FACTOR BETA RECEPTOR INHIB
E4	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR INTER
E5	3		TRANSFORMING GROWTH FACTOR BETA RECEPTOR KINAS
E6	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR MESSE
E7	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR TGF-B
E8	25	1	TRANSFORMING GROWTH FACTOR BETA RECEPTOR TYPE
E9	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR V
E10	40		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 1
E11	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 1 KIN
E12	133	5	TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2

Enter P or PAGE for more

? p

Ref	Items	RT	Index-term
E13	2		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2 --D
E14	65		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2 --E
E15	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2 --I
E16	3		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2 --P
E17	1		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 2 MES
E18	7		TRANSFORMING GROWTH FACTOR BETA RECEPTOR 3
E19	2		TRANSFORMING GROWTH FACTOR BETA RECEPTOR (S)
E20	32	3	TRANSFORMING GROWTH FACTOR BETA RECEPTORS
E21	1		TRANSFORMING GROWTH FACTOR BETA REGULATORY ELE
E22	1		TRANSFORMING GROWTH FACTOR BETA RELATED PROTEI
E23	2		TRANSFORMING GROWTH FACTOR BETA RESPONSE ELEME
E24	1		TRANSFORMING GROWTH FACTOR BETA RESPONSIVE ELE

Enter P or PAGE for more

? p

Ref	Items	Index-term
E25	1	TRANSFORMING GROWTH FACTOR BETA RI
E26	1	TRANSFORMING GROWTH FACTOR BETA RII
E27	1	TRANSFORMING GROWTH FACTOR BETA RIL
E28	1	TRANSFORMING GROWTH FACTOR BETA SECRETION
E29	1	TRANSFORMING GROWTH FACTOR BETA SIGNAL MEDIATO
E30	2	TRANSFORMING GROWTH FACTOR BETA SIGNAL TRANSDU
E31	6	TRANSFORMING GROWTH FACTOR BETA SIGNALING
E32	5	TRANSFORMING GROWTH FACTOR BETA SIGNALING PATH
E33	1	TRANSFORMING GROWTH FACTOR BETA SIGNALLING PAT
E34	1	TRANSFORMING GROWTH FACTOR BETA SIMULATED CLON
E35	1	TRANSFORMING GROWTH FACTOR BETA SOLUBLE RECEPT
E36	4	TRANSFORMING GROWTH FACTOR BETA STIMULATED CLO

Enter P or PAGE for more

?

? e transforming growth factor beta IV

Ref	Items	RT	Index-term
E1	1		TRANSFORMING GROWTH FACTOR BETA ISOFORM OVEREX
E2	3		TRANSFORMING GROWTH FACTOR BETA ISOFORMS
E3	0		*TRANSFORMING GROWTH FACTOR BETA IV
E4	1		TRANSFORMING GROWTH FACTOR BETA L
E5	1	1	TRANSFORMING GROWTH FACTOR BETA LATENCY ASSOCI
E6	1		TRANSFORMING GROWTH FACTOR BETA LATENCY BINDIN
E7	1		TRANSFORMING GROWTH FACTOR BETA LIKE BINDING P
E8	9		TRANSFORMING GROWTH FACTOR BETA MASKING PROTEI
E9	1		TRANSFORMING GROWTH FACTOR BETA MEMBER
E10	4		TRANSFORMING GROWTH FACTOR BETA MESSENGER RNA
E11	1		TRANSFORMING GROWTH FACTOR BETA MONOCLONAL ANT
E12	1		TRANSFORMING GROWTH FACTOR BETA MONONUCLEAR MA

Enter P or PAGE for more

? e tgfb4

Ref	Items	Index-term
E1	1	TGFB3/MSX1 MARKERS
E2	1	TGFB3VARIANT
E3	21	*TGFB4
E4	1	TGFB47
E5	1	TGFB5
E6	8	TGFC
E7	1	TGFCARS
E8	1	TGFCDIA
E9	2	TGFCYS
E10	1	TGFCYSSUP33SER
E11	1	TGFCYS33
E12	2	TGFCYS33SER

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?

? s e3

S2 21 'TGFB4'

? e tgfb-4

Ref	Items	Index-term
E1	3	TGFB-3
E2	3	TGFB-3R

E3 0 *TGFB-4
E4 1 TGFB/G1
E5 5 TGFBA
E6 2 TGFBA
E7 1 TGFBATTA1
E8 1 TGFBBA1
E9 1 TGFBBETA
E10 1 TGFBBETA1
E11 1 TGFBBR2
E12 4 TGFB

Enter P or PAGE for more

? p

Ref	Items	Index-term
E13	3	TGFBETAT
E14	1	TGFBETATA1
E15	1	TGFBETAT1
E16	3	TGFBEP
E17	1	TGFBET
E18	14995	TGFBETA
E19	1	TGFBETA ACTIVATED KINASE TAK1 TRANSFORMING GRO
E20	1	TGFBETA BETA RECEPTOR TYPE II
E21	1	TGFBETA EXPRESSION
E22	2	TGFBETA FAMILY
E23	1	TGFBETA FAMILY SIGNALING
E24	1	TGFBETA GROWTH FACTOR

Enter P or PAGE for more

? p

Ref	Items	Index-term
E25	1	TGFBETA HP75 CELLS
E26	1	TGFBETA INDUCED CLONE H3
E27	1	TGFBETA INHIBITOR TUMOR GROWTH FACTOR BETA INH
E28	1	TGFBETA ISOFORMS
E29	1	TGFBETA MODULATION
E30	8	TGFBETA RECEPTOR
E31	1	TGFBETA RECEPTOR I
E32	1	TGFBETA RECEPTOR II
E33	12	TGFBETA RECEPTORS
E34	4	TGFBETA SIGNAL TRANSDUCTION
E35	11	TGFBETA SIGNALING
E36	1	TGFBETA SIGNALING PATHWAY

Enter P or PAGE for more

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Ref	Items	Index-term
E37	1	TGFBETA SIGNALING PATHWAYS
E38	6	TGFBETA SIGNALLING
E39	1	TGFBETA SIGNALS
E40	1	TGFBETA STEROID RECEPTORS
E41	6	TGFBETA SUPERFAMILY
E42	1	TGFBETA TRANSFORMING GROWTH FACTOR BETA
E43	1	TGFBETA TRANSFORMING GROWTH FACTOR BETA TRANSF
E44	2	TGFBETA TYPE I RECEPTOR
E45	3	TGFBETA TYPE II RECEPTOR
E46	1	TGFBETA TYPE II RECEPTOR PROMOTER
E47	1	TGFBETA TYPE II RECEPTOR SIGNALING
E48	1	TGFBETA VARIANTS

Enter P or PAGE for more

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Ref Items Index-term
E49 2 TGFBETA(TRANSFORMING GROWTH FACTOR BETA)
E50 1 TGFBETA)

? s e48

S3 1 'TGFBETA VARIANTS'

? p

Ref Items Index-term
E1 1 TGFBETA)
E2 1 TGFBETA- 1
E3 2 TGFBETA-DEPENDENT
E4 1 TGFBETA-IIR
E5 1 TGFBETA-INDEPENDENT
E6 2 TGFBETA- INDUCED
E7 1 TGFBETA- INDUCIBLE GENE H3 (BETAIG-H3)
E8 1 TGFBETA- PATHWAY
E9 1 TGFBETA-RECEPTOR INTERACTING PROTEIN-1
E10 3 TGFBETA-RII
E11 1 TGFBETA-RII CELL LINE (HOMINIDAE)
E12 1 TGFBETA-SIGNALING

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? p

Ref Items Index-term
E13 1 TGFBETA-SIGNALLING
E14 2 TGFBETA-SUPERFAMILY
E15 1 TGFBETA-TREATED
E16 7 TGFBETA-1
E17 1 TGFBETA-1 LASER MICRODISSECTION
E18 1 TGFBETA-1 TRANSFORMING GROWTH FACTOR BETA-1
E19 3 TGFBETA-2
E20 1 TGFBETA-3
E21 2 TGFBETA, TRANSFORMING GROWTH FACTOR BETA
E22 1 TGFBETA, TRANSFORMING GROWTH FACTOR-BETA
E23 2 TGFBETAA
E24 1 TGFBETAAND

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Ref Items Index-term
E25 3 TGFBETABETA1
E26 2 TGFBETAB2
E27 1 TGFBETACALCITROIL
E28 11 TGFBETAC10
E29 11 TGFBETAC25
E30 1 TGFBETAEPSILON
E31 1 TGFBETAFNSHOWED
E32 1 TGFBETAFNSKELETAL
E33 1 TGFBETAFNTREATMENT
E34 36 TGFBETAI
E35 1 TGFBETAIGH3
E36 20 TGFBETAI

Enter P or PAGE for more

? p

Ref	Items	Index-term
E37	1	TGFBETAIII
E38	38	TGFBETAIIR
E39	1	TGFBETAIN
E40	430	TGFBETAINF
E41	12	TGFBETAINF 1
E42	1	TGFBETAINF 3
E43	1	TGFBETAINF 4
E44	7	TGFBETAIR
E45	1	TGFBETASOFORMS
E46	16	TGFBETAL
E47	1	TGFBETAMU
E48	1	TGFBETAOVER

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Ref	Items	Index-term
E49	3	TGFBETAP
E50	2	TGFBETAPRII

? p

Ref	Items	Index-term
E1	2	TGFBETAPRII
E2	113	TGFBETAR
E3	1	TGFBETAR II (A) 10
E4	1	TGFBETAR II (GT) 3
E5	7	TGFBETARE
E6	1	TGFBETARECEPTER
E7	2	TGFBETARECEPTOR
E8	1	TGFBETARECEPTORS
E9	1	TGFBETARES
E10	123	TGFBETARI
E11	610	TGFBETARII
E12	1	TGFBETARII FRAMESHIFT MUTATION

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Ref	Items	Index-term
E13	5	TGFBETARIIDELTAKD
E14	16	TGFBETARIIII
E15	7	TGFBETARS
E16	1	TGFBETARSUB1
E17	20	TGFBETAR1
E18	4	TGFBETAR11
E19	30	TGFBETAR2
E20	10	TGFBETAR3
E21	446	TGFBETAS
E22	4	TGFBETASFR2
E23	1	TGFBETASIGNALING
E24	1	TGFBETASL

Enter P or PAGE for more

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Ref	Items	Index-term
E25	3	TGFBETASR
E26	7	TGFBETASRII
E27	183	TGFBETASUB1

E28 1 TGFBETASUB1STIMULATED
E29 40 TGFBETASUB2
E30 1 TGFBETASUB2TGFBETASUB2
E31 17 TGFBETASUB3
E32 3 TGFBETASUP
E33 1 TGFBETASUPERFAMILY
E34 1 TGFBETASUPPRESSED
E35 4 TGFBETASUP1
E36 4 TGFBETAS1

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Ref Items Index-term
E37 1 TGFBETATGFBETA
E38 1 TGFBETATO
E39 3 TGFBETATYPE
E40 7500 TGFBETA1
E41 1 TGFBETA1 - TRANSFORMING GROWTH FACTOR BETA
E42 1 TGFBETA1 DIFFERENTIATION
E43 1 TGFBETA1 GENE
E44 1 TGFBETA1 mRNA
E45 1 TGFBETA1 OVEREXPRESSION
E46 1 TGFBETA1 RECEPTORS
E47 1 TGFBETA1-ACTIVATED
E48 1 TGFBETA1ALPHAMP

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Ref Items Index-term
E49 1 TGFBETA1ANGIOTENSINII
E50 1 TGFBETA1AVAILABILITY
? p

Ref Items Index-term
E1 1 TGFBETA1AVAILABILITY
E2 1 TGFBETA1CDNA
E3 1 TGFBETA1DURING
E4 1 TGFBETA1GENE
E5 1 TGFBETA1KIDNEY
E6 1 TGFBETA1L
E7 2 TGFBETA1LAP
E8 4 TGFBETA1MRNA
E9 2 TGFBETA1POSITIVE
E10 1 TGFBETA1PRODUCING
E11 11 TGFBETA1R
E12 1 TGFBETA1REQUIRE

Enter P or PAGE for more

? p

Ref Items Index-term
E13 7 TGFBETA1RI
E14 7 TGFBETA1RII
E15 6 TGFBETA1SUP
E16 2 TGFBETA1SUPS223
E17 2 TGFBETA1SUPWT
E18 1 TGFBETA1SUP32
E19 1 TGFBETA1TRANSGENE
E20 1 TGFBETA1WERE

E21 1402 TGFBETA2
E22 1 TGFBETA2, IL-1
E23 1 TGFBETA2HUMAN
E24 5 TGFBETA2R

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? p

Ref Items Index-term
E25 14 TGFBETA2SUP
E26 934 TGFBETA3
E27 1 TGFBETA3-ELISA
E28 1 TGFBETA3R
E29 1 TGFBETA3RII
E30 10 TGFBETA3SUP
E31 30 TGFBETA4
E32 14 TGFBETA5
E33 2 TGFBETE
E34 1 TGFBETGA1
E35 1 TGFBGR
E36 375 TGFB1

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? s e31
S4 30 'TGFBETA4'
? p

Ref Items Index-term
E37 1 TGFB1 (BETA 1G-H3) GENE
E38 1 TGFB1 (BIGH3) GENE
E39 5 TGFB1 BIGH3 GENE
E40 15 TGFB1 GENE
E41 1 TGFB1 TRANSFORMING GROWTH FACTOR-BETA-1
E42 1 TGFB1(BIGH3) GENE
E43 1 TGFB1-INDUCED
E44 2 TGFBIGENE
E45 9 TGFBII
E46 1 TGFBIII
E47 6 TGFBIIIR
E48 44 TGFBIIIR

Enter P or PAGE for more

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Ref Items Index-term
E49 1 TGFBIIIR GENE
E50 1 TGFBINDUCES
? p

Ref Items Index-term
E1 1 TGFBINDUCES
E2 7 TGFBINF
E3 2 TGFBIN3
E4 19 TGFBIP
E5 7 TGFBKM2
E6 2 TGFBKM2SUP129
E7 2 TGFBKM2129
E8 11 TGFBBL
E9 7 TGFBM1
E10 6 TGFBM3
E11 25 TGFBP

E12 1 TGFBP-3

Enter P or PAGE for more

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Ref	Items	Index-term
E13	2	TGFBPS
E14	1	TGFBP1
E15	1	TGFBP3
E16	1	TGFBP4
E17	1	TGFBP5
E18	27	TGFBR
E19	1	TGFBR-SMAD
E20	1	TGFBR-SMAD SUPERFAMILY
E21	11	TGFBRAP1
E22	11	TGFBRAP1 PROTEIN, HUMAN
E23	21	TGFBR1
E24	111	TGFBR1I

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? s e16

S5 1 'TGFBP4'

? p

Ref	Items	Index-term
E25	1	TGFBR1I GENE
E26	1	TGFBR1I GENE TRANSFORMING GROWTH FACTOR-BETA R
E27	3	TGFBR1L
E28	2	TGFBRLOXP
E29	1	TGFBRMRNA
E30	6	TGFBR1
E31	6	TGFBR2
E32	1	TGFBR3
E33	2	TGFBRTA
E34	163	TGFBR1
E35	1	TGFBR1 GENE
E36	1	TGFBR1 KINASE

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Ref	Items	Index-term
E37	1	TGFBR1 TRANSFORMING GROWTH FACTOR, BETA RECEPT
E38	4	TGFBR1-ASTERISK-6A
E39	1	TGFBR1-6A ALLELE
E40	2	TGFBR16A
E41	463	TGFBR2
E42	9	TGFBR2 GENE
E43	1	TGFBR2 GENE TYPE II TRANSFORMING GROWTH FACTOR
E44	13	TGFBR2 PROTEIN, HUMAN
E45	2	TGFBR2-RESTORED
E46	1	TGFBR2FLOXE2
E47	2	TGFBR2FLX
E48	4	TGFBR2FSPKO

Enter P or PAGE for more

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Ref	Items	Index-term
E49	1	TGFBR2HEPKO
E50	1	TGFBR2L

? e lefty 1

Ref	Items	Index-term
E1	1	LEFTY SIGNALING
E2	1	LEFTY VENTRICULAR REMODELING
E3	0	*LEFTY 1
E4	1	LEFTY 1 PROTEIN
E5	1	LEFTY- 1
E6	4	LEFTY-A
E7	1	LEFTY-A ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
E8	1	LEFTY-A mRNA
E9	1	LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
E10	2	LEFTY-B
E11	1	LEFTY-DEPENDENT
E12	1	LEFTY-GENE RELATED PRODUCT

Enter P or PAGE for more

? s e4-e10

	1	LEFTY 1 PROTEIN
	1	LEFTY- 1
	4	LEFTY-A
	1	LEFTY-A ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
	1	LEFTY-A mRNA
	1	LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
	2	LEFTY-B
S6	8	E4-E10

? p

Ref	Items	Index-term
E13	1	LEFTY-RELATED
E14	1	LEFTY-SIGNALING
E15	13	LEFTY-1
E16	5	LEFTY-1 GENE
E17	1	LEFTY-1 PROTEIN
E18	12	LEFTY-2
E19	3	LEFTY-2 GENE
E20	1	LEFTY-2 ISOLATION
E21	1	LEFTY-2 PROTEIN
E22	34	LEFTYA
E23	1	LEFTYA GENE
E24	1	LEFTYA PROTEIN

Enter P or PAGE for more

? s e15 or e17 or e18 or e20 or e21 or e22 or e24

	13	LEFTY-1
	1	LEFTY-1 PROTEIN
	12	LEFTY-2
	1	LEFTY-2 ISOLATION
	1	LEFTY-2 PROTEIN
	34	LEFTYA
	1	LEFTYA PROTEIN
S7	57	'LEFTY-1' OR 'LEFTY-1 PROTEIN' OR 'LEFTY-2' OR 'LEFTY-2 ISOLATION' OR 'LEFTY-2 PROTEIN' OR 'LEFTYA' OR 'LEFTYA PROTEIN'

? p

Ref	Items	Index-term
E25	2	LEFTYB
E26	1	LEFTYB PROTEIN
E27	5	LEFTYL
E28	1	LEFTYRAY

E29 2 LEFTYS
E30 204 LEFTY1
E31 3 LEFTY1 GENE
E32 1 LEFTY1 PROTEIN
E33 1 LEFTY1GENE
E34 6 LEFTY1LEFTY2
E35 1 LEFTY1LEFTY2 TUBULIN MUTANT
E36 4 LEFTY1SUP

Enter P or PAGE for more

? s e25-e26 or e30 or e32 or e34 or e35 or e36

2 LEFTYB
1 LEFTYB PROTEIN
204 LEFTY1
1 LEFTY1 PROTEIN
6 LEFTY1LEFTY2
1 LEFTY1LEFTY2 TUBULIN MUTANT
4 LEFTY1SUP

S8 206 E25-E26 OR E30 OR E32 OR E34 OR E35 OR E36

? p

Ref Items Index-term
E37 196 LEFTY2
E38 3 LEFTY2 GENE
E39 1 LEFTY2 PROTEIN
E40 1 LEFTY2GENE
E41 1 LEFTY3
E42 1 LEFTY69
E43 4 LEFT1
E44 1 LEFU
E45 91 LEFUA
E46 1 LEFUA (OSTEICHTHYES)
E47 6 LEFUA COSTATA
E48 6 LEFUA COSTATA (OSTEICHTHYES)

Enter P or PAGE for more

? s e37 or e39

196 LEFTY2
1 LEFTY2 PROTEIN
S9 196 'LEFTY2' OR 'LEFTY2 PROTEIN'

? p

Ref Items Index-term
E49 1 LEFUA COSTATA ECHIGONIA
E50 1 LEFUA COSTATA MITOCHONDRIAL D-LOOP REGION GENE
? e lefty a

Ref Items Index-term
E1 929 LEFTY
E2 1 *LEFTY A
E3 6 LEFTY GENE
E4 1 LEFTY KREH'S ULTIMATE GUIDE TO FLY FISHING (BO
E5 2 LEFTY MUTANTS
E6 1 LEFTY POPULATION
E7 155 LEFTY PROTEIN
E8 1 LEFTY PROTEIN FAMILY
E9 4 LEFTY PROTEINS
E10 1 LEFTY SECRETED FACTORS
E11 1 LEFTY SEQUENCE
E12 1 LEFTY SIGNALING

Enter P or PAGE for more
? s e2 or e7 or e8 or e9
1 LEFTY A
155 LEFTY PROTEIN
1 LEFTY PROTEIN FAMILY
4 LEFTY PROTEINS
S10 161 'LEFTY A' OR 'LEFTY PROTEIN' OR 'LEFTY PROTEIN FAMILY' OR
'LEFTY PROTEINS'

? p

Ref	Items	Index-term
E13	1	LEFTY VENTRICULAR REMODELING
E14	1	LEFTY 1 PROTEIN
E15	1	LEFTY- 1
E16	4	LEFTY-A
E17	1	LEFTY-A ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
E18	1	LEFTY-A mRNA
E19	1	LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
E20	2	LEFTY-B
E21	1	LEFTY-DEPENDENT
E22	1	LEFTY-GENE RELATED PRODUCT
E23	1	LEFTY-RELATED
E24	1	LEFTY-SIGNALING

Enter P or PAGE for more
? s e14 or e15 or e16 or e17 or e18 or e19 or e20
1 LEFTY 1 PROTEIN
1 LEFTY- 1
4 LEFTY-A
1 LEFTY-A ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
1 LEFTY-A mRNA
1 LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR
2 LEFTY-B
S11 8 'LEFTY 1 PROTEIN' OR 'LEFTY- 1' OR 'LEFTY-A' OR 'LEFTY-A
ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR' OR 'LEFTY-A mRNA'
OR 'LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR' OR
'LEFTY-B'

? ds

Set	Items	Description
S1	3	'TRANSFORMING GROWTH FACTOR BETA ISOFORMS'
S2	21	'TGFB4'
S3	1	'TGFBETA VARIANTS'
S4	30	'TGFBETA4'
S5	1	'TGFBP4'
S6	8	E4-E10
S7	57	'LEFTY-1' OR 'LEFTY-1 PROTEIN' OR 'LEFTY-2' OR 'LEFTY-2 IS- OLATION' OR 'LEFTY-2 PROTEIN' OR 'LEFTYA' OR 'LEFTYA PROTEIN'
S8	206	E25-E26 OR E30 OR E32 OR E34 OR E35 OR E36
S9	196	'LEFTY2' OR 'LEFTY2 PROTEIN'
S10	161	'LEFTY A' OR 'LEFTY PROTEIN' OR 'LEFTY PROTEIN FAMILY' OR - 'LEFTY PROTEINS'
S11	8	'LEFTY 1 PROTEIN' OR 'LEFTY- 1' OR 'LEFTY-A' OR 'LEFTY-A E- NDOMETRIAL BLEEDING-ASSOCIATED FACTOR' OR 'LEFTY-A mRNA' OR '- LEFTY-A/ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR' OR 'LEFTY-B'

?

? s s1 or s2 or s3 or s4 or s5 or s6 or s7 or s8 or s9 or s10 or s11

3	S1
21	S2
1	S3
30	S4

1 S5
8 S6
57 S7
206 S8
196 S9
161 S10
8 S11
S12 531 S1 OR S2 OR S3 OR S4 OR S5 OR S6 OR S7 OR S8 OR S9 OR S10
OR S11

? s s12/1996:2005

Processing

Processed 10 of 26 files ...
>>>One or more prefixes are unsupported
>>> or undefined in one or more files.

>>>Year ranges not supported in one or more files

Processing

Completed processing all files

531 S12
49727561 PY=1996 : PY=2005
S13 525 S12/1996:2005

? s s12 not s13

531 S12
525 S13
S14 6 S12 NOT S13

?

? rd

...completed examining records
S15 4 RD (unique items)

? t s15/6/all

15/6/1 (Item 1 from file: 71)
00304408 95125590

The immunomodulatory diversity of the proteins of the transforming growth factor beta (TGFbetaP) family

PUBLICATION DATE: 19950000

15/6/2 (Item 2 from file: 71)
00290512 95107663

Expression of transforming growth factor beta in the embryonic avian lens coincides with the presence of mitochondria

PUBLICATION DATE: 19950000

15/6/3 (Item 1 from file: 144)

10488633 PASCAL No.: 92-0692127

Localization of the human insulin-like growth-factor-binding protein 4 gene to chromosomal region 17q12-21.1
1992

15/6/4 (Item 1 from file: 399)

DIALOG(R) File 399:(c) 2005 American Chemical Society. All rts. reserv.

Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid encoding transforming growth factor .beta. 4 from chicken embryo chondrocytes

? t s15/9/1 2 3

15/9/1 (Item 1 from file: 71)

DIALOG(R) File 71:ELSEVIER BIOBASE
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00304408 95125590

The immunomodulatory diversity of the proteins of the transforming growth factor beta (TGFbetaP) family

Wieczorek Z.; Sion J.; Kluczyk A.; Zbozien R.; Stafanowicz P.; Siemion I.Z.
ADDRESS: Z. Wieczorek, L. Hirschfeld Inst Immun/Exp Therapy, Polish Academy
of Sciences, Czerska 12, 53-114 Wroclaw, Poland

Journal: International Journal of Peptide and Protein Research, 46/2
(113-118), 1995, Denmark

PUBLICATION DATE: 19950000

CODEN: IJPPC

ISSN: 0367-8377

DOCUMENT TYPE: Article

LANGUAGES: English SUMMARY LANGUAGES: English

The examination of immunomodulatory properties of oligopeptides derived from two exposed loops (containing thymopentin-like and tuftsin-like sequences, respectively) of the proteins belonging to TGFbeta family suggests that the particular species of the TGFbeta family should differ distinctly in their influence on the immune response. According to our results obtained from three TGFbeta species of mammals, TGFbeta 2 should be a strong immunosuppressor, whereas for TGFbeta 3 the immunostimulative potency is more probable. TGFbeta 1 species would possess both immunosuppressive and immunostimulative potency, residing in two different loops of the protein. The results obtained also suggest that chicken TGFbeta4 should be associated with immunostimulative effects and xenopus TGFbeta5 with immunosuppressive ones.

DESCRIPTORS:

Peptide immunomodulators; Thymopentin-like sequences; Transforming growth factor beta; Tuftsin-like sequences

CLASSIFICATION CODE AND DESCRIPTION:

89.2.4.5 - CELL AND DEVELOPMENTAL BIOLOGY / CELL GROWTH AND DIVISION /
Growth Factors and Inhibitors / Transforming growth factors (TGF)

86.5.4.6 - IMMUNOLOGY AND INFECTIOUS DISEASES / HUMORAL MEDIATORS OF IMMUNE
RESPONSE / Other Factors / Haematopoietic growth factors (CSF)

15/9/2 (Item 2 from file: 71)

DIALOG(R) File 71:ELSEVIER BIOBASE

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00290512 95107663

Expression of transforming growth factor beta in the embryonic avian lens
coincides with the presence of mitochondria

Potts J.D.; Bassnett S.; Beebe D.C.

ADDRESS: J.D. Potts, Department of Anatomy/Cell Biology, Uniformed Svcs.
Univ. of Health Sci., 4301 Jones Bridge Road, Bethesda, MD
20814-4799, United States

Journal: Developmental Dynamics, 203/3 (317-323), 1995, United States

PUBLICATION DATE: 19950000

CODEN: DEDYE

ISSN: 1058-8388

DOCUMENT TYPE: Article

LANGUAGES: English SUMMARY LANGUAGES: English

During their maturation, lens cells lose all membrane bound organelles,
including mitochondria. In chicken embryos this process begins in the

central lens fibers beginning around embryonic day 12 (E12). Transforming growth factor beta (TGF β) is a multipotent growth modulator thought to play a role in numerous developmental processes. TGF β 1 has been localized to mitochondria in rat liver cells and muscle cells. In the present study, we examined the expression of TGF β isoform mRNAs and proteins during chicken embryonic lens development. PCR analysis demonstrated TGF β 2 and TGF β 3 transcripts in the lens epithelium and fibers throughout pre- and post-hatching development. TGF β isoforms were detected throughout the lens epithelium and fibers early in development (E6). However by E19, the distribution of TGF β 2 and TGF β 3 transcripts and proteins coincided with regions of the lens that contained mitochondria. In addition, intense TGF β staining was observed in the basal portions of the equatorial epithelial cells, a region with abundant mitochondria. Transcripts for TGF β 1 and TGF β 4 were not detected in any tissue or time frame examined. Similarly, no immunostaining for TGF β 1 was observed.

DESCRIPTORS:

TGF β ; Chicken lens; Lens differentiation; Mitochondria

CLASSIFICATION CODE AND DESCRIPTION:

89.8.9.7 - CELL AND DEVELOPMENTAL BIOLOGY / DEVELOPMENT (BY TISSUE AND ORGAN SYSTEMS) / Nervous System / Sensory - visual
89.2.4.5 - CELL AND DEVELOPMENTAL BIOLOGY / CELL GROWTH AND DIVISION / Growth Factors and Inhibitors / Transforming growth factors (TGF)
89.1.8.7 - CELL AND DEVELOPMENTAL BIOLOGY / MEMBRANES AND CELL TRANSPORT / Cytoplasmic Membranes / Mitochondria

15/9/3 (Item 1 from file: 144)

DIALOG(R) File 144:Pascal
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10488633 PASCAL No.: 92-0692127
Localization of the human insulin-like growth-factor-binding protein 4 gene to chromosomal region 17q12-21.1
BAJALICA S; ALLANDER S V; EHRENBORG E; BRONDUM-NIELSEN K; LUTHMAN H; LARSSON C
Karolinska hosp., dep. clinical genetics, 10401 Stockholm, Sweden
Journal: Human genetics, 1992, 89 (2) 234-236
ISSN: 0340-6717 CODEN: HUGEDQ Availability: INIST-2672;
354000028118920170
No. of Refs.: 13 ref.
Document Type: P (Serial) ; A (Analytic)
Country of Publication: Federal Republic of Germany
Language: English
Insulin-like growth-factor-binding proteins (IGFBPs) constitute a family of structurally related proteins that specifically bind insulin-like growth factors and modulate their functions. In this study, the chromosomal localization was determined for the gene encoding IGFBP4, i.e. inhibitory-IGFBP. A polymerase chain reaction (PCR) fragment corresponding to the previously published cDNA sequence was used to isolate overlapping cosmid clones. By fluorescent in situ hybridization to metaphase chromosomes, the TGFBP4 gene was then localized to chromosomal region 17q21-21.1

English Descriptors: E17-Chromosome; Binding protein; Genetic mapping; Human; Somatomedin C; Insulin like growth factor 2; Polymerase chain reaction; Molecular hybridization; In situ; Molecular biology; Genetics; Exploration

French Descriptors: Chromosome E17; Proteine liaison; Carte genetique; Homme; Somatomedine C; Facteur croissance IGF2; Reaction chaine polymerase; Hybridation moleculaire; In situ; Biologie moleculaire; Genetique; Exploration

Classification Codes: 002A07C03

? t s15/9/4

15/9/4 (Item 1 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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111091468 CA: 111(11)91468h JOURNAL
Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid encoding transforming growth factor .beta. 4 from chicken embryo chondrocytes

AUTHOR(S): Jakowlew, Sonia B.; Dillard, Pamela J.; Sporn, Michael B.; Roberts, Anita B.

LOCATION: Lab. Chemoprev., Natl. Cancer Inst., Bethesda, MD, 20892, USA
JOURNAL: Mol. Endocrinol. DATE: 1988 VOLUME: 2 NUMBER: 12 PAGES:

1186-95 CODEN: MOENEN ISSN: 0888-8809 LANGUAGE: English

SECTION:

CA203003 Biochemical Genetics

CA202XXX Mammalian Hormones

CA213XXX Mammalian Biochemistry

IDENTIFIERS: cDNA cloning sequencing chicken TGFbeta4, transforming growth factor chicken gene sequence

DESCRIPTORS:

Gene and Genetic element,animal...

for transforming growth factor .beta.4, of chicken, nucleotide and encoded peptide sequences of

Animal growth regulators,.beta.4-transforming growth factors...

gene for, of chicken, nucleotide and encoded peptide sequences of Deoxyribonucleic acid sequences,.beta.4-transforming growth factor-specifying...
of chicken, multiple clones, complete

Protein sequences...

of transforming growth factor .beta.4 and precursor, multiple clones, complete

Molecular cloning...

of transforming growth factor .beta.4 cDNA, of chicken
Chicken...

transforming growth factor .beta.4 gene of, nucleotide and encoded peptide sequences of

CAS REGISTRY NUMBERS:

122319-69-1 122319-70-4 amino acid sequence of

122318-73-4 nucleotide sequence of

? logoff hold

26sep05 07:24:19 User228206 Session D2511.2
\$2.83 0.832 DialUnits File155
\$2.83 Estimated cost File155
\$5.35 0.907 DialUnits File5
\$5.35 Estimated cost File5
\$29.30 1.323 DialUnits File34
\$29.30 Estimated cost File34
\$0.87 0.211 DialUnits File35
\$0.87 Estimated cost File35
\$1.06 0.198 DialUnits File48
\$1.06 Estimated cost File48
\$5.17 1.378 DialUnits File65

\$5.17 Estimated cost File65
\$5.25 0.600 DialUnits File71
\$0.00 2 Type(s) in Format 6
\$4.00 2 Type(s) in Format 9
\$4.00 4 Types
\$9.25 Estimated cost File71
\$7.54 0.709 DialUnits File73
\$7.54 Estimated cost File73
\$0.38 0.089 DialUnits File91
\$0.38 Estimated cost File91
\$1.93 0.553 DialUnits File94
\$1.93 Estimated cost File94
\$0.87 0.205 DialUnits File98
\$0.87 Estimated cost File98
\$0.81 0.150 DialUnits File135
\$0.81 Estimated cost File135
\$3.68 0.819 DialUnits File144
\$0.00 1 Type(s) in Format 6
\$1.65 1 Type(s) in Format 9
\$1.65 2 Types
\$5.33 Estimated cost File144
\$1.14 0.259 DialUnits File149
\$1.14 Estimated cost File149
\$1.77 0.300 DialUnits File156
\$1.77 Estimated cost File156
\$0.95 0.300 DialUnits File159
\$0.95 Estimated cost File159
\$0.89 0.198 DialUnits File162
\$0.89 Estimated cost File162
\$0.45 0.130 DialUnits File164
\$0.45 Estimated cost File164
\$1.45 0.136 DialUnits File172
\$1.45 Estimated cost File172
\$0.29 0.082 DialUnits File266
\$0.29 Estimated cost File266
\$0.43 0.123 DialUnits File369
\$0.43 Estimated cost File369
\$0.36 0.102 DialUnits File370
\$0.36 Estimated cost File370
\$13.95 1.112 DialUnits File399
\$0.55 1 Type(s) in Format 6
\$2.75 1 Type(s) in Format 9
\$3.30 2 Types
\$17.25 Estimated cost File399
\$2.57 0.116 DialUnits File434
\$2.57 Estimated cost File434
\$0.33 0.068 DialUnits File444
\$0.33 Estimated cost File444
\$0.61 0.096 DialUnits File467
\$0.61 Estimated cost File467
OneSearch, 26 files, 10.996 DialUnits FileOS
\$2.66 TELNET
\$101.84 Estimated cost this search
\$101.84 Estimated total session cost 11.207 DialUnits

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Search for

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NCBI BLAST program reference [PMID:[9254694](#)]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query: 15 AA

Date run: 2005-09-24 15:42:21 UTC+0100 on sib-gm1.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,312,053 sequences; 758,486,757 total letters

UniProt Knowledgebase Release 6.0 consists of:

UniProtKB/Swiss-Prot Release 48.0 of 13-Sep-2005: 194317 entries

UniProtKB/TrEMBL Release 31.0 of 13-Sep-2005: 2105517 entries

List of potentially matching sequences

Send selected sequences to

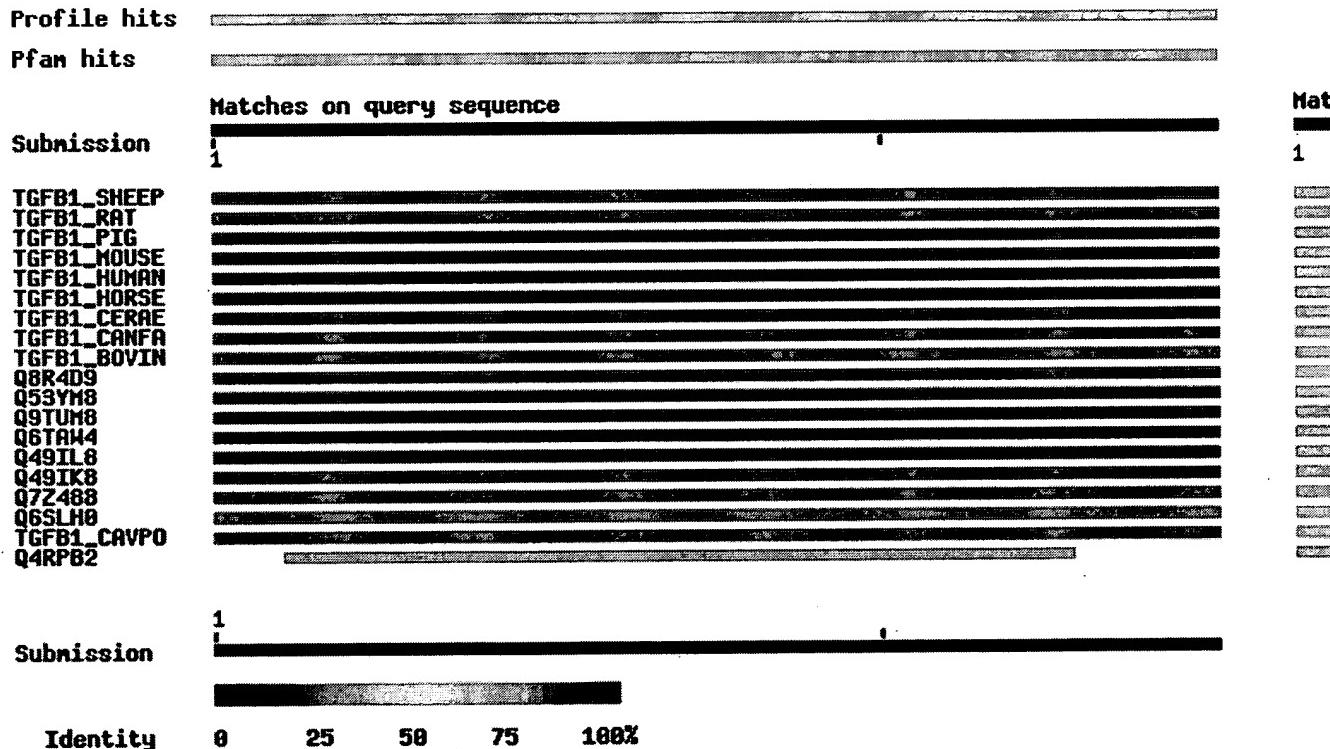
Include query sequence

Db AC	Description	Score	E-value
<input type="checkbox"/> sp P50414 TGFB1_SHEEP	Transforming growth factor beta 1 precursor...	53	6e-07
<input type="checkbox"/> sp P17246 TGFB1_RAT	Transforming growth factor beta 1 precursor ...	53	6e-07
<input type="checkbox"/> sp P07200 TGFB1_PIG	Transforming growth factor beta 1 precursor ...	53	6e-07
<input type="checkbox"/> sp P04202 TGFB1_MOUSE	Transforming growth factor beta 1 precursor...	53	6e-07
<input type="checkbox"/> sp P01137 TGFB1_HUMAN	Transforming growth factor beta 1 precursor...	53	6e-07
<input type="checkbox"/> sp O19011 TGFB1_HORSE	Transforming growth factor beta 1 precursor...	53	6e-07
<input type="checkbox"/> sp P09533 TGFB1_CERAEE	Transforming growth factor beta 1 precursor...	53	6e-07
<input type="checkbox"/> sp P54831 TGFB1_CANFA	Transforming growth factor beta 1 precursor...	53	6e-07
<input type="checkbox"/> sp P18341 TGFB1_BOVIN	Transforming growth factor beta 1 precursor...	53	6e-07

- tr Q8R4D9 _SIGHI Transforming growth factor beta-1 protein (Fragm... 53 6e-07
- tr Q53YM8 _RAT TGF beta 1 [Rattus norvegicus (Rat)] 53 6e-07
- tr Q9TUM8 _HORSE Transforming growth factor beta 1 [TGFb1] [Equus... 53 6e-07
- tr Q6TAW4 _FELCA TGF beta (Fragment) [Felis silvestris catus (Cat)] 53 6e-07
- tr Q49IL8 _HUMAN Transforming growth factor beta 1 precursor (Fra... 53 6e-07
- tr Q49IK8 _HUMAN Transforming growth factor beta 1 precursor (Fra... 53 6e-07
- tr Q7Z488 _HUMAN Transforming growth factor beta 1 precursor (Fra... 53 6e-07
- tr Q6SLH0 _PERMA Transforming growth factor beta 1 (Fragment) [Tg... 50 5e-06
- sp Q9Z1Y6 TGFB1_CAVPO Transforming growth factor beta 1 precurs... 50 7e-06
- tr Q4RPB2 _TETNG Chromosome 1 SCAF15008, whole genome shotgun seq... 32 2.1

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
 (© [Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)



Alignments

sp P50414	Transforming growth factor beta 1 precursor (TGF-beta 1)	390
TGFB1_SHEEP	[TGFB1]	AA
	[Ovis aries (Sheep)]	<u>align</u>

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 99 PEADYYAKEVTRVLM 113

sp P17246 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_RAT [Tgfb1] AA
 [Rattus norvegicus (Rat)] align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 99 PEADYYAKEVTRVLM 113

sp P07200 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_PIG [TGFB1] AA
 [Sus scrofa (Pig)] align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 99 PEADYYAKEVTRVLM 113

sp P04202 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_MOUSE [Tgfb1] AA
 [Mus musculus (Mouse)] align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 99 PEADYYAKEVTRVLM 113

sp P01137 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_HUMAN [TGFB1] AA
 [Homo sapiens (Human)] align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 99 PEADYYAKEVTRVLM 113

sp O19011 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_HORSE [TGFB1]
[Equus caballus (Horse)] AA align

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp P09533 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_CERAE [TGFB1]
[Cercopithecus aethiops (Green monkey) (Grivet)] AA align

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp P54831 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_CANFA [TGFB1]
[Canis familiaris (Dog)] AA align

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 99 PEADYYAKEVTRVLM 113

sp P18341 Transforming growth factor beta 1 precursor (TGF-beta 1) 315 AA
TGFB1_BOVIN (Fragment) [TGFB1] [Bos taurus (Bovine)] align

Score = 53.2 bits (118), Expect = 6e-07
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
PEADYYAKEVTRVLM
Sbjct: 24 PEADYYAKEVTRVLM 38

tr Q8R4D9 Transforming growth factor beta-1 protein (Fragment) 368
 Q8R4D9 SIGHI [Tgfb1] AA
 [Sigmodon hispidus (Hispid cotton rat)] align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 77 PEADYYAKEVTRVLM 91

tr Q53YM8 TGF beta 1 [Rattus norvegicus (Rat)] 390 AA
 Q53YM8 RAT align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 99 PEADYYAKEVTRVLM 113

tr Q9TUM8 Transforming growth factor beta 1 [TGFb1] [Equus 390
 Q9TUM8 HORSE caballus (Horse)] AA align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 99 PEADYYAKEVTRVLM 113

tr Q6TAW4 TGF beta (Fragment) [Felis silvestris catus (Cat)] 226 AA
 Q6TAW4 FELCA align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 50 PEADYYAKEVTRVLM 64

tr Q49IL8 Transforming growth factor beta 1 precursor (Fragment) 118
 Q49IL8 HUMAN [TGFB1] AA align
 [Homo sapiens (Human)]

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 99 PEADYYAKEVTRVLM 113

tr Q49IK8 Transforming growth factor beta 1 precursor (Fragment) 118
 Q49IK8_HUMAN [TGFB1] AA
 [Homo sapiens (Human)] align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 99 PEADYYAKEVTRVLM 113

tr Q7Z488 Transforming growth factor beta 1 precursor (Fragment) 118
 Q7Z488_HUMAN [TGFB1] AA
 [Homo sapiens (Human)] align

Score = 53.2 bits (118), Expect = 6e-07
 Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 1 PEADYYAKEVTRVLM 15
 PEADYYAKEVTRVLM
 Sbjct: 99 PEADYYAKEVTRVLM 113

tr Q6SLH0 Transforming growth factor beta 1 (Fragment) [Tgfb1] 249
 Q6SLH0_PERMA [Peromyscus AA
 maniculatus (Deer mouse)] align

Score = 50.3 bits (111), Expect = 5e-06
 Identities = 14/15 (93%), Positives = 14/15 (93%)

Query: 1 PEADYYAKEVTRVLM 15
 PE DYYAKEVTRVLM
 Sbjct: 65 PETDYYAKEVTRVLM 79

sp Q9Z1Y6 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_CAVPO [TGFB1] AA
 [Cavia porcellus (Guinea pig)] align

Score = 49.8 bits (110), Expect = 7e-06
 Identities = 14/15 (93%), Positives = 14/15 (93%)

Query: 1 PEADYYAKEVTRVLM 15
 PE DYYAKEVTRVLM
 Sbjct: 99 PEPDYYAKEVTRVLM 113

tr Q4RPB2 Chromosome 1 SCAF15008, whole genome shotgun sequence. 454
 Q4RPB2_TETNG (Fragment) AA
 [GSTENG00031190001] [Tetraodon nigroviridis (Green align
 puffer)]

Score = 31.6 bits (67), Expect = 2.1
 Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 2 EADYYAKEVTRV 13
 E DYYAKEV R+
 Sbjct: 96 EEDYYAKEVQRI 107

Database: EXPASY/UniProtKB
 Posted date: Sep 12, 2005 12:34 PM
 Number of letters in database: 758,486,757
 Number of sequences in database: 2,312,053

Lambda K H
 0.329 0.280 1.74

Gapped
 Lambda K H
 0.294 0.110 0.610

Matrix: PAM30
 Gap Penalties: Existence: 9, Extension: 1
 Number of HSP's successfully gapped in prelim test: 0
 length of query: 15
 length of database: 758,486,757
 effective HSP length: 6
 effective length of query: 9
 effective length of database: 744,614,439
 effective search space: 6701529951
 effective search space used: 6701529951
 T: 16
 A: 40
 X1: 15 (7.1 bits)
 X2: 35 (14.8 bits)
 X3: 58 (24.6 bits)
 S1: 42 (21.8 bits)
 S2: 62 (29.5 bits)

Wallclock time: 2 seconds

ESVEPEPEP

sp|P50414|TGFB1_SHEEP
sp|O19011|TGFB1_HORSE
sp|P18341|TGFB1_BOVIN
sp|P09531|TGFB1_CHICK

GQILSKLRLASPPSQGDVPPGPLPEAILALYNSTRDRVAG-ESAETEPEP
GQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRAQVAG-ESAETEPEP
-----AILALYNSTRDRVAG-ESAETEPEP
GQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLKQRARLRPPPDK

: *****:

sp|P07200|TGFB1_PIG

EADYYAKEVTRVLMLESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVL

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QHVELYQKYS NNS

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Choose the appropriate BLAST  program and  database:

blastp - query against the UniProt Knowledgebase (Swiss-Prot + TrEMBL)

 Taxonomic groups (not available for PDB and translated EST):

select a
database
subsection

To restrict the search to a particular taxon, it is much faster to select from the drop-down list on the left than to specify your own taxonomic group, which will give you more accurate statistics.

or specify
a
taxonomic
group

Enter a species name, a TaxID or the latin name of a taxonomic group (separated by new
OX lines) to restrict your search to a particular taxon. You may enter several names separated by
";"). Example: Fungi; Homo sapiens.

or select a
microbial
proteome

AB TO
 epatozid
 Boening
 ag 5/10

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tblastn - query against the six-frame translation of a nucleotide database

Taxonomic groups:

or select a microbial genome

✉ Your email address:

If an e-mail address is provided, results will be automatically mailed back (recommended for tblastn searches).

or

Options:

- ⌚ Comparison Matrix: Auto-select
- Number of best scoring sequences to show:
- Number of best alignments to show:
- ⌚ Setting the E threshold: (Number of expected matches in a random database)
- ⌚ Filter the sequence for low-complexity regions
- ⌚ Gapped alignment
- ⌚ Identity BLAST

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NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 13 AA

Date run: 2005-09-24 15:53:30 UTC+0100 on sib-gm1.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,312,053 sequences; 758,486,757 total letters

UniProt Knowledgebase Release 6.0 consists of:

UniProtKB/Swiss-Prot Release 48.0 of 13-Sep-2005: 194317 entries

UniProtKB/TrEMBL Release 31.0 of 13-Sep-2005: 2105517 entries

Taxonomic view	NiceBlast view	Printable view
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List of potentially matching sequences

Send selected sequences to	Clustal W (multiple alignment)	<input type="button" value="Submit Query"/>
<input type="button" value="Select up to..."/>		

Include query sequence

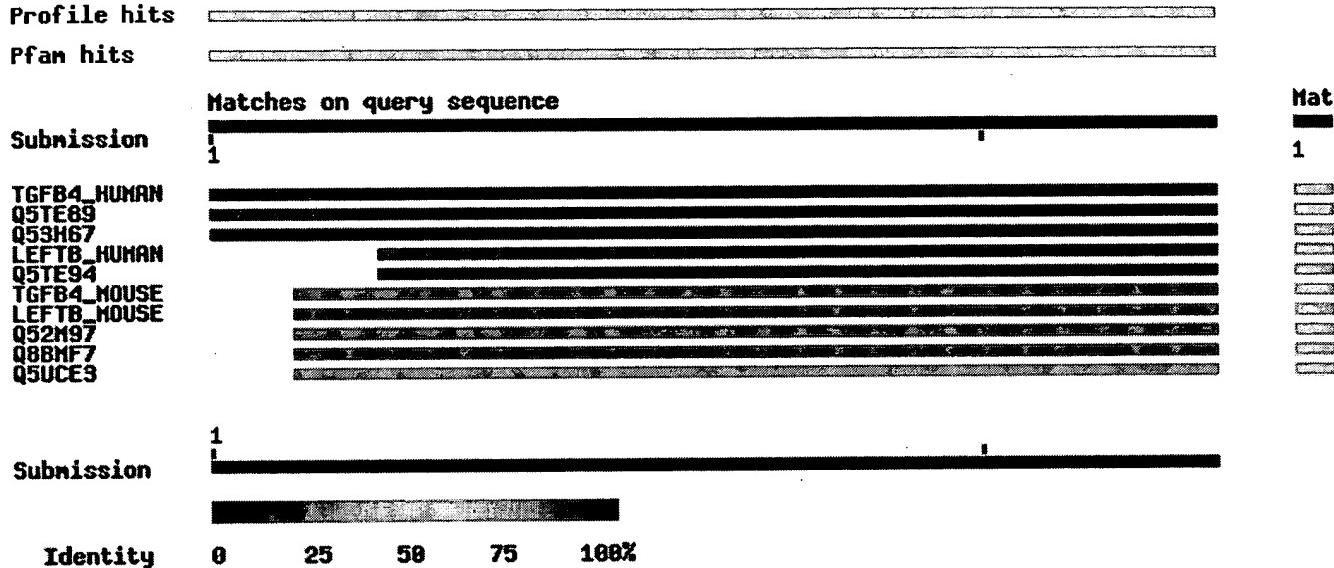
Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp_O00292	TGFB4_HUMAN Transforming growth factor beta 4 precursor...	43	6e-04
<input type="checkbox"/>	tr_Q5TE89	_HUMAN Left-right determination factor 2 [LEFTY2] [Homo...	43	6e-04
<input type="checkbox"/>	tr_Q53H67	_HUMAN Left-right determination, factor B preproprotein...	43	6e-04
<input type="checkbox"/>	sp_O75610	LEFTB_HUMAN Left-right determination factor B precursor...	38	0.019
<input type="checkbox"/>	tr_Q5TE94	_HUMAN Left-right determination factor 1 [LEFTY1] [Homo...	38	0.019
<input type="checkbox"/>	sp_Q64280	TGFB4_MOUSE Transforming growth factor beta 4 precursor...	38	0.025
<input type="checkbox"/>	sp_P57785	LEFTB_MOUSE Left-right determination factor B precursor...	38	0.025
<input type="checkbox"/>	tr_Q52M97	_XENLA Hypothetical protein [Xenopus laevis (African cl...	38	0.025
<input type="checkbox"/>	tr_Q8BMF7	_MOUSE Mus musculus 13 days embryo male testis cDNA, RI...	38	0.025

tr Q5UCE3 _RAT EBAF precursor [Rattus norvegicus (Rat)]

35 0.20

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
 ([? Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)



Alignments

sp 000292 Transforming growth factor beta 4 precursor (TGF-beta 4) 366 AA
 TGFB4_HUMAN (Endometrial bleeding-associated factor) (Left-right determination factor A) (Lefty-A protein) [EBAF] [Homo sapiens (Human)]

Score = 43.5 bits (95), Expect = 6e-04
 Identities = 13/13 (100%), Positives = 13/13 (100%)

Query: 1 ASEASTHLLVFGM 13
 ASEASTHLLVFGM
 Sbjct: 91 ASEASTHLLVFGM 103

tr Q5TE89 Left-right determination factor 2 [LEFTY2] [Homo sapiens 366 AA
 Q5TE89_HUMAN (Human)]

Score = 43.5 bits (95), Expect = 6e-04
 Identities = 13/13 (100%), Positives = 13/13 (100%)

Query: 1 ASEASTHLLVFGM 13
 ASEASTHLLVFGM
 Sbjct: 91 ASEASTHLLVFGM 103

tr Q53H67 Left-right determination, factor B preproprotein variant 366
Q53H67_HUMAN (Fragment) AA
[LEFTY1] [Homo sapiens (Human)] align

Score = 43.5 bits (95), Expect = 6e-04
Identities = 13/13 (100%), Positives = 13/13 (100%)

Query: 1 ASEASTHLLVFGM 13
ASEASTHLLVFGM
Sbjct: 91 ASEASTHLLVFGM 103

sp O75610 Left-right determination factor B precursor (Lefty-B 366
LEFTB_HUMAN protein) AA
[LEFTB] [Homo sapiens (Human)] align

Score = 38.4 bits (83), Expect = 0.019
Identities = 11/11 (100%), Positives = 11/11 (100%)

Query: 3 EASTHLLVFGM 13
EASTHLLVFGM
Sbjct: 93 EASTHLLVFGM 103

tr Q5TE94 Left-right determination factor 1 [LEFTY1] [Homo sapiens 366
Q5TE94_HUMAN (Human)] AA align

Score = 38.4 bits (83), Expect = 0.019
Identities = 11/11 (100%), Positives = 11/11 (100%)

Query: 3 EASTHLLVFGM 13
EASTHLLVFGM
Sbjct: 93 EASTHLLVFGM 103

sp Q64280 Transforming growth factor beta 4 precursor (TGF-beta 4) 368
TGFB4_MOUSE (Lefty AA
protein) (Lefty-1 protein) (STRA3 protein) [Ebaft] [Mus align
musculus (Mouse)]

Score = 38.0 bits (82), Expect = 0.025
Identities = 11/12 (91%), Positives = 11/12 (91%)

Query: 2 SEASTHLLVFGM 13
SE STHLLVFGM
Sbjct: 92 SETSTHLLVFGM 103

sp P57785 Left-right determination factor B precursor (Lefty-2
LEFTB_MOUSE protein)
[Leftb] [Mus musculus (Mouse)] 368
AA
align

Score = 38.0 bits (82), Expect = 0.025
Identities = 11/12 (91%), Positives = 11/12 (91%)

Query: 2 SEASTHLLVFGM 13
SE STHLLVFGM
Sbjct: 92 SETSTHLLVFGM 103

tr Q52M97 Hypothetical protein [Xenopus laevis (African clawed
Q52M97_XENLA frog)] 368
AA
align

Score = 38.0 bits (82), Expect = 0.025
Identities = 11/12 (91%), Positives = 11/12 (91%)

Query: 2 SEASTHLLVFGM 13
SE STHLLVFGM
Sbjct: 92 SETSTHLLVFGM 103

tr Q8BMF7 Mus musculus 13 days embryo male testis cDNA, RIKEN
Q8BMF7_MOUSE full-length 368
enriched library, clone:6030463A22 product:LEFT-RIGHT
DETERMINATION FACTOR B (LEFTY-2 PROTEIN), full insert
sequence (Left-right determination factor 2) [Lefty2]
[Mus musculus (Mouse)] AA
align

Score = 38.0 bits (82), Expect = 0.025
Identities = 11/12 (91%), Positives = 11/12 (91%)

Query: 2 SEASTHLLVFGM 13
SE STHLLVFGM
Sbjct: 92 SETSTHLLVFGM 103

tr Q5UCE3 EBAF precursor [Rattus norvegicus (Rat)] 366 AA
Q5UCE3_RAT
align

Score = 35.0 bits (75), Expect = 0.20
Identities = 10/12 (83%), Positives = 10/12 (83%)

Query: 2 SEASTHLLVFGM 13
SE S HLLVFGM
Sbjct: 92 SETSSHLLVFGM 103

Database: EXPASY/UniProtKB
Posted date: Sep 12, 2005 12:34 PM

Number of letters in database: 758,486,757
Number of sequences in database: 2,312,053

Lambda K H
0.342 0.277 1.67

Gapped

Lambda K H
0.294 0.110 0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of HSP's successfully gapped in prelim test: 0

length of query: 13

length of database: 758,486,757

effective HSP length: 4

effective length of query: 9

effective length of database: 749,238,545

effective search space: 6743146905

effective search space used: 6743146905

T: 16

A: 40

X1: 15 (7.4 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 40 (21.6 bits)

S2: 62 (29.5 bits)

Wallclock time: 2 seconds

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Search for

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In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:[9254694](#)]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 13 AA

Date run: 2005-09-24 15:46:19 UTC+0100 on sib-gm1.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,312,053 sequences; 758,486,757 total letters

UniProt Knowledgebase Release 6.0 consists of:

UniProtKB/Swiss-Prot Release 48.0 of 13-Sep-2005: 194317 entries

UniProtKB/TrEMBL Release 31.0 of 13-Sep-2005: 2105517 entries

List of potentially matching sequences

Send selected sequences to

Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp_P07200	TGFB1_PIG Transforming growth factor beta 1 precursor ...	46	9e-05
<input type="checkbox"/>	sp_P01137	TGFB1_HUMAN Transforming growth factor beta 1 precursor...	42	0.001
<input type="checkbox"/>	sp_P09533	TGFB1_CERAЕ Transforming growth factor beta 1 precursor...	42	0.001
<input type="checkbox"/>	sp_P54831	TGFB1_CANFA Transforming growth factor beta 1 precursor...	42	0.001
<input type="checkbox"/>	tr_Q6TAW4	_FELCA TGF beta (Fragment) [Felis silvestris catus (Cat)]	42	0.001
<input type="checkbox"/>	tr_Q49IL8	_HUMAN Transforming growth factor beta 1 precursor (Fra...	42	0.001
<input type="checkbox"/>	tr_Q49IK8	_HUMAN Transforming growth factor beta 1 precursor (Fra...	42	0.001
<input type="checkbox"/>	tr_Q7Z488	_HUMAN Transforming growth factor beta 1 precursor (Fra...	42	0.001
<input type="checkbox"/>	sp_P17246	TGFB1_RAT Transforming growth factor beta 1 precursor ...	40	0.008

<input type="checkbox"/>	sp <u>P04202</u> <u>TGFB1_MOUSE</u> Transforming growth factor beta 1 precursor...	<u>40</u>	0.008
<input type="checkbox"/>	tr <u>Q8R4D9</u> <u>SIGHI</u> Transforming growth factor beta-1 protein (Fragment)	<u>40</u>	0.008
<input type="checkbox"/>	tr <u>Q53YM8</u> <u>RAT</u> TGF beta 1 [Rattus norvegicus (Rat)]	<u>40</u>	0.008
<input type="checkbox"/>	sp <u>Q9Z1Y6</u> <u>TGFB1_CAVPO</u> Transforming growth factor beta 1 precursor...	<u>39</u>	0.014
<input type="checkbox"/>	sp <u>P50414</u> <u>TGFB1_SHEEP</u> Transforming growth factor beta 1 precursor...	<u>37</u>	0.045
<input type="checkbox"/>	sp <u>O19011</u> <u>TGFB1_HORSE</u> Transforming growth factor beta 1 precursor...	<u>37</u>	0.045
<input type="checkbox"/>	sp <u>P18341</u> <u>TGFB1_BOVIN</u> Transforming growth factor beta 1 precursor...	<u>37</u>	0.045
<input type="checkbox"/>	tr <u>Q9TUM8</u> <u>HORSE</u> Transforming growth factor beta 1 [TGFb1] [Equus...]	<u>37</u>	0.045
<input type="checkbox"/>	tr <u>Q6SLH0</u> <u>PERMA</u> Transforming growth factor beta 1 (Fragment) [Tg...]	<u>37</u>	0.061
<input type="checkbox"/>	tr <u>Q68FX4</u> <u>RAT</u> Hematopoietic cell specific Lyn substrate 1 (Predi...)	<u>34</u>	0.48
<input type="checkbox"/>	tr <u>Q6T890</u> <u>ACTPL</u> TonB2 [tonB2] [Actinobacillus pleuropneumoniae (...]	<u>33</u>	0.64
<input type="checkbox"/>	tr <u>Q4R7C6</u> <u>MACFA</u> Testis cDNA, clone: QtsA-15617, similar to human...	<u>33</u>	0.64
<input type="checkbox"/>	sp <u>P14317</u> <u>HCLS1_HUMAN</u> Hematopoietic lineage cell specific protei...	<u>33</u>	0.86
<input type="checkbox"/>	tr <u>Q61BK9</u> <u>HUMAN</u> HCLS1 protein [HCLS1] [Homo sapiens (Human)]	<u>33</u>	0.86
<input type="checkbox"/>	tr <u>Q53Y93</u> <u>HUMAN</u> Hematopoietic cell-specific Lyn substrate 1 [Hom...]	<u>33</u>	0.86
<input type="checkbox"/>	tr <u>Q87MK6</u> <u>VIBPA</u> Hypothetical protein VP2226 [VP2226] [Vibrio par...]	<u>32</u>	1.1
<input type="checkbox"/>	tr <u>Q9EN57</u> <u>NPVST</u> Zinc finger protein [Spodoptera litura multicaps...]	<u>32</u>	1.5
<input type="checkbox"/>	tr <u>Q91BL1</u> <u>NPVST</u> HOAR [Spodoptera litura multicapsid nucleopolyhe...]	<u>32</u>	1.5
<input type="checkbox"/>	tr <u>Q8BGM6</u> <u>MOUSE</u> Mus musculus 10 days neonate cerebellum cDNA, RI...	<u>32</u>	1.5
<input type="checkbox"/>	tr <u>Q80Z30</u> <u>RAT</u> Calmodulin-dependent protein kinase phosphatase N ...	<u>32</u>	1.5
<input type="checkbox"/>	tr <u>Q5SX30</u> <u>MOUSE</u> Protein phosphatase 1E (PP2C domain containing) ...	<u>32</u>	1.5
<input type="checkbox"/>	tr <u>Q80VJ8</u> <u>MOUSE</u> Hypothetical protein BC050196 [BC050196] [Mus mu...]	<u>32</u>	2.1
<input type="checkbox"/>	tr <u>Q6CE67</u> <u>YARLI</u> Similarity [YALI0B18172g] [Yarrowia lipolytica (...]	<u>32</u>	2.1
<input type="checkbox"/>	tr <u>Q9VT49</u> <u>DROME</u> CG14168-PA [CG14168] [Drosophila melanogaster (F...]	<u>31</u>	2.8
<input type="checkbox"/>	tr <u>P91156</u> <u>CAEEL</u> Hypothetical protein [C43E11.1] [Caenorhabditis ...]	<u>31</u>	2.8
<input type="checkbox"/>	tr <u>Q5KGJ5</u> <u>CRYNE</u> Hypothetical protein [CNE03390] [Cryptococcus ne...]	<u>31</u>	2.8
<input type="checkbox"/>	tr <u>Q55S44</u> <u>CRYNE</u> Hypothetical protein [CNBE3380] [Cryptococcus ne...]	<u>31</u>	2.8
<input type="checkbox"/>	tr <u>Q8I4T3</u> <u>PLAF7</u> PFG377 protein [PFL2405c] [Plasmodium falciparum...]	<u>31</u>	3.7
<input type="checkbox"/>	tr <u>Q26022</u> <u>PLAFA</u> Plasmodium falciparum sexual stage mRNA sequence...	<u>31</u>	3.7
<input type="checkbox"/>	tr <u>Q25857</u> <u>PLAFA</u> Pfg377 [Plasmodium falciparum]	<u>31</u>	3.7
<input type="checkbox"/>	tr <u>Q7S935</u> <u>NEUCR</u> Predicted protein [NCU07949.1] [Neurospora crassa]	<u>31</u>	3.7
<input type="checkbox"/>	tr <u>Q52FL1</u> <u>MAGGR</u> Hypothetical protein [MG01625.4] [Magnaporthe gr...]	<u>31</u>	3.7
<input type="checkbox"/>	sp <u>Q9D1X0</u> <u>NOL3_MOUSE</u> Nucleolar protein 3 [Nol3] [Mus musculus (M...]	<u>30</u>	5.0
<input type="checkbox"/>	sp <u>Q8XRH0</u> <u>FTSK1_RALSO</u> DNA translocase ftsK 1 [ftsK1] [Ralstonia ...]	<u>30</u>	5.0
<input type="checkbox"/>	sp <u>Q9GLM6</u> <u>APOE_HYLLA</u> Apolipoprotein E precursor (Apo-E) [APOE] [...]	<u>30</u>	5.0
<input type="checkbox"/>	tr <u>Q8R2S3</u> <u>MOUSE</u> Nucleolar protein 3 [Nol3] [Mus musculus (Mouse)]	<u>30</u>	5.0
<input type="checkbox"/>	tr <u>Q8C550</u> <u>MOUSE</u> Mus musculus adult male hypothalamus cDNA, RIKEN...	<u>30</u>	5.0
<input type="checkbox"/>	tr <u>Q53YU5</u> <u>MOUSE</u> Apoptosis repressor interacting with CARD (0 day...)	<u>30</u>	5.0
<input type="checkbox"/>	tr <u>Q73XH7</u> <u>MYCPA</u> Fas [fas] [Mycobacterium paratuberculosis]	<u>30</u>	5.0
<input type="checkbox"/>	tr <u>Q478V8</u> <u>9RHOO</u> Response regulator receiver:CheW-like protein:AT...	<u>30</u>	5.0
<input type="checkbox"/>	tr <u>Q9EXU1</u> <u>KLEPN</u> TonB (Fragment) [tonB] [Klebsiella pneumoniae]	<u>30</u>	5.0
<input type="checkbox"/>	tr <u>Q6XXM0</u> <u>MYCSM</u> Fatty acid synthetase I [fas1] [Mycobacterium sm...]	<u>30</u>	5.0
<input type="checkbox"/>	tr <u>Q5MBX2</u> <u>ACTSU</u> TonB2 [tonB2] [Actinobacillus suis]	<u>30</u>	5.0
<input type="checkbox"/>	tr <u>Q4QZC1</u> <u>KLEPN</u> Periplasmic energy transducer (Fragment) [tonB] ...	<u>30</u>	5.0
<input type="checkbox"/>	tr <u>Q9VAI5</u> <u>DROME</u> CG15506-PB, isoform B [CG15506] [Drosophila mela...]	<u>30</u>	5.0

<input type="checkbox"/>	tr	Q9N411	CAEEL Prion-like-(Q/n-rich)-domain-bearing protein pro...	30	5.0
<input type="checkbox"/>	tr	Q8MZB6	DROME AT15667p [CG15506] [Drosophila melanogaster (Fru...]	30	5.0
<input type="checkbox"/>	tr	Q8IMK6	DROME CG15506-PA, isoform A [CG15506] [Drosophila mela...]	30	5.0
<input type="checkbox"/>	tr	Q4U8R9	THEAN Hypothetical protein [TA10045] [Theileria annulata]	30	5.0
<input type="checkbox"/>	tr	Q5AQG7	EMENI Hypothetical protein [AN9463.2] [Aspergillus nid...]	30	5.0
<input type="checkbox"/>	tr	Q5ARP0	EMENI Predicted protein [AN9040.2] [Aspergillus nidula...]	30	5.0
<input type="checkbox"/>	tr	Q5ATE5	EMENI Hypothetical protein [AN8435.2] [Aspergillus nid...]	30	5.0
<input type="checkbox"/>	tr	Q527B1	MAGGR Hypothetical protein [MG06645.4] [Magnaporthe gr...]	30	5.0
<input type="checkbox"/>	tr	Q526E4	MAGGR Hypothetical protein [MG06862.4] [Magnaporthe gr...]	30	5.0
<input type="checkbox"/>	tr	Q4PFF2	USTMA Hypothetical protein [UM01161.1] [Ustilago maydi...]	30	5.0
<input type="checkbox"/>	tr	Q4IFF5	GIBZE Hypothetical protein [FG04053.1] [Gibberella zea...]	30	5.0
<input type="checkbox"/>	sp	P26185	TONB_SERMA TonB protein [tonB] [Serratia marcescens]	30	6.7
<input type="checkbox"/>	sp	P25945	TONB_SALTY TonB protein [tonB] [Salmonella typhimurium]	30	6.7
<input type="checkbox"/>	sp	P45610	TONB_KLEPN TonB protein [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	sp	P46383	TONB_ENTAE TonB protein [tonB] [Enterobacter aerogenes...]	30	6.7
<input type="checkbox"/>	sp	P02929	TONB_ECOLI TonB protein [tonB] [Escherichia coli]	30	6.7
<input type="checkbox"/>	sp	Q62881	NOL3_RAT Nucleolar protein 3 [Nol3] [Rattus norvegicus...]	30	6.7
<input type="checkbox"/>	sp	P97855	G3BP_MOUSE Ras-GTPase-activating protein binding prote...	30	6.7
<input type="checkbox"/>	tr	Q4SUQ6	TETNG Chromosome undetermined SCAF13844, whole genome ...	30	6.7
<input type="checkbox"/>	tr	Q62882	RAT Hypothetical protein [Rattus norvegicus (Rat)]	30	6.7
<input type="checkbox"/>	tr	Q5NCU1	MOUSE Ras-GTPase-activating protein SH3-domain binding...	30	6.7
<input type="checkbox"/>	tr	Q571F9	MOUSE MKIAA4115 protein (Fragment) [G3bp] [Mus musculu...]	30	6.7
<input type="checkbox"/>	tr	Q57P65	SALCH SsrAB activated gene [srfA] [Salmonella cholerae...]	30	6.7
<input type="checkbox"/>	tr	Q57NS2	SALCH Energy transducer; uptake of iron, cyanocobalimi...	30	6.7
<input type="checkbox"/>	tr	Q9S3M6	BORPE TonB protein (Siderophore-mediated iron transpor...	30	6.7
<input type="checkbox"/>	tr	Q8Z7E4	SALTI TonB protein [tonB] [Salmonella typhi]	30	6.7
<input type="checkbox"/>	tr	Q8XCC2	ECO57 Energy transducer; uptake of iron, cyanocobalimi...	30	6.7
<input type="checkbox"/>	tr	Q8FHW5	ECOL6 TonB protein [tonB] [Escherichia coli O6]	30	6.7
<input type="checkbox"/>	tr	Q885B3	PSESM Major facilitator family transporter [PSPTO1922]...	30	6.7
<input type="checkbox"/>	tr	Q884X6	PSESM Flagellar assembly protein Flih, putative [PSPTO...]	30	6.7
<input type="checkbox"/>	tr	Q83RM7	SHIFL Membrane protein, energy transducer [tonB] [Shig...]	30	6.7
<input type="checkbox"/>	tr	Q7WKX3	BORBR Siderophore-mediated iron transport protein [ton...]	30	6.7
<input type="checkbox"/>	tr	Q7W7I4	BORPA Siderophore-mediated iron transport protein [ton...]	30	6.7
<input type="checkbox"/>	tr	Q5PHV4	SALPA Putative virulence effector protein [srfA] [Salm...]	30	6.7
<input type="checkbox"/>	tr	Q5PCS7	SALPA TonB protein [tonB] [Salmonella paratyphi-a]	30	6.7
<input type="checkbox"/>	tr	Q5NZS1	AZOSE Translation initiation factor IF-2 [infB] [Azoar...]	30	6.7
<input type="checkbox"/>	tr	Q48GE4	PSESH Flagellar assembly protein Flih [fliH] [Pseudomo...]	30	6.7
<input type="checkbox"/>	tr	Q9ZG18	BORBR TonB [tonB] [Bordetella bronchiseptica (Alcalige...]	30	6.7
<input type="checkbox"/>	tr	Q9S3Z9	KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9S3Z7	KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9S3Z6	KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9R440	KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9R427	KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9R426	KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7
<input type="checkbox"/>	tr	Q9EXU0	KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae]	30	6.7

tr Q9EXT9 _KLEPN TonB (Fragment) [tonB] [Klebsiella pneumoniae] 30 6.7

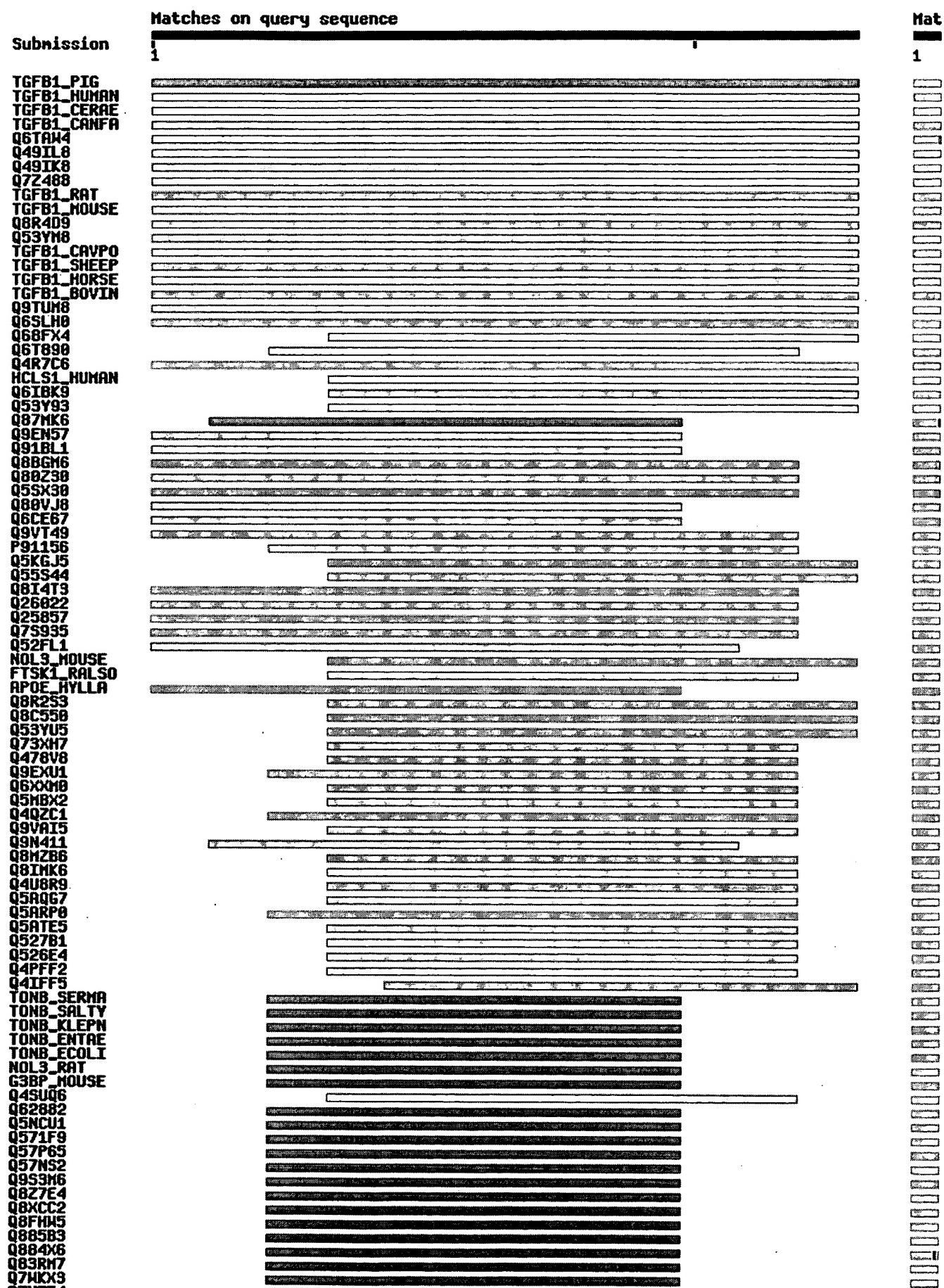
Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

( [Help](#)) ([use ScanProsite](#) for more details about PROSITE matches)

Profile hits 

Pfam hits 



Alignments

sp P07200 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_PIG [TGFB1] AA
 [Sus scrofa (Pig)] align

Score = 46.0 bits (101), Expect = 9e-05
 Identities = 13/13 (100%), Positives = 13/13 (100%)

Query: 1 ESVEPEPEPEADY 13
 ESVEPEPEPEADY
 Sbjct: 91 ESVEPEPEPEADY 103

sp P01137 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_HUMAN [TGFB1] AA
 [Homo sapiens (Human)] align

Score = 42.2 bits (92), Expect = 0.001
 Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEADY 13
 ES EPEPEPEADY
 Sbjct: 91 ESAEPEPEPEADY 103

sp P09533 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_CERAE [TGFB1] AA
 [Cercopithecus aethiops (Green monkey) (Grivet)] align

Score = 42.2 bits (92), Expect = 0.001
 Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEADY 13
 ES EPEPEPEADY
 Sbjct: 91 ESAEPEPEPEADY 103

sp P54831 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_CANFA [TGFB1] AA
 [Canis familiaris (Dog)] align

Score = 42.2 bits (92), Expect = 0.001
 Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEADY 13
 ES EPEPEPEADY
 Sbjct: 91 ESAEPEPEPEADY 103

tr Q6TAW4 TGF beta (Fragment) [Felis silvestris catus (Cat)] 226 AA
Q6TAW4 _FELCA

align

Score = 42.2 bits (92), Expect = 0.001
 Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEREADY 13
 ES EPEPEPEREADY
 Sbjct: 42 ESAEPEPEPEREADY 54

tr Q49IL8 Transforming growth factor beta 1 precursor (Fragment) 118
Q49IL8 _HUMAN [TGFB1] AA
 [Homo sapiens (Human)] align

Score = 42.2 bits (92), Expect = 0.001
 Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEREADY 13
 ES EPEPEPEREADY
 Sbjct: 91 ESAEPEPEPEREADY 103

tr Q49IK8 Transforming growth factor beta 1 precursor (Fragment) 118
Q49IK8 _HUMAN [TGFB1] AA
 [Homo sapiens (Human)] align

Score = 42.2 bits (92), Expect = 0.001
 Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEREADY 13
 ES EPEPEPEREADY
 Sbjct: 91 ESAEPEPEPEREADY 103

tr Q7Z488 Transforming growth factor beta 1 precursor (Fragment) 118
Q7Z488 _HUMAN [TGFB1] AA
 [Homo sapiens (Human)] align

Score = 42.2 bits (92), Expect = 0.001
 Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 1 ESVEPEPEPEREADY 13
 ES EPEPEPEREADY
 Sbjct: 91 ESAEPEPEPEREADY 103

sp P17246 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1 _RAT [Tgfb1] AA
 [Rattus norvegicus (Rat)] align

Score = 39.7 bits (86), Expect = 0.008
Identities = 11/13 (84%), Positives = 12/13 (91%)

Query: 1 ESVEPEPEPEREADY 13
ES +PEPEPEREADY
Sbjct: 91 ESADPEPEPEREADY 103

sp P04202 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_MOUSE [Tgfb1]
[Mus musculus (Mouse)] AA align

Score = 39.7 bits (86), Expect = 0.008
Identities = 11/13 (84%), Positives = 12/13 (91%)

Query: 1 ESVEPEPEPEREADY 13
ES +PEPEPEREADY
Sbjct: 91 ESADPEPEPEREADY 103

tr Q8R4D9 Transforming growth factor beta-1 protein (Fragment) 368
Q8R4D9_SIGHI [Tgfb1]
[Sigmodon hispidus (Hispid cotton rat)] AA align

Score = 39.7 bits (86), Expect = 0.008
Identities = 11/13 (84%), Positives = 12/13 (91%)

Query: 1 ESVEPEPEPEREADY 13
ES +PEPEPEREADY
Sbjct: 69 ESADPEPEPEREADY 81

tr Q53YM8 TGF beta 1 [Rattus norvegicus (Rat)] 390 AA
Q53YM8_RAT align

Score = 39.7 bits (86), Expect = 0.008
Identities = 11/13 (84%), Positives = 12/13 (91%)

Query: 1 ESVEPEPEPEREADY 13
ES +PEPEPEREADY
Sbjct: 91 ESADPEPEPEREADY 103

sp Q9Z1Y6 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
TGFB1_CAVPO [TGFB1]
[Cavia porcellus (Guinea pig)] AA align

Score = 38.8 bits (84), Expect = 0.014
Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 1 ESVEPEPEPEREADY 13
 ES EPEPEPE DY
 Sbjct: 91 ESAEPEPEPEPDY 103

sp P50414 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_SHEEP [TGFB1]
 [Ovis aries (Sheep)] AA align

Score = 37.1 bits (80), Expect = 0.045
 Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 1 ESVEPEPEPEREADY 13
 ES E EPEREADY
 Sbjct: 91 ESAETEPEPEREADY 103

sp Q19011 Transforming growth factor beta 1 precursor (TGF-beta 1) 390
 TGFB1_HORSE [TGFB1]
 [Equus caballus (Horse)] AA align

Score = 37.1 bits (80), Expect = 0.045
 Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 1 ESVEPEPEPEREADY 13
 ES E EPEREADY
 Sbjct: 91 ESAETEPEPEREADY 103

sp P18341 Transforming growth factor beta 1 precursor (TGF-beta 1) 315 AA
 TGFB1_BOVIN (Fragment) [TGFB1] [Bos taurus (Bovine)] align

Score = 37.1 bits (80), Expect = 0.045
 Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 1 ESVEPEPEPEREADY 13
 ES E EPEREADY
 Sbjct: 16 ESAETEPEPEREADY 28

tr Q9TUM8 Transforming growth factor beta 1 [TGFB1] [Equus 390
 Q9TUM8_HORSE caballus (Horse)] AA align

Score = 37.1 bits (80), Expect = 0.045
 Identities = 11/13 (84%), Positives = 11/13 (84%)

Query: 1 ESVEPEPEPEREADY 13
 ES E EPEREADY
 Sbjct: 91 ESAETEPEPEREADY 103

tr Q6SLH0 Transforming growth factor beta 1 (Fragment) [Tgfb1] 249
 Q6SLH0_PERMA [Peromyscus
 maniculatus (Deer mouse)] AA
align

Score = 36.7 bits (79), Expect = 0.061
 Identities = 10/13 (76%), Positives = 11/13 (83%)

Query: 1 ESVEPEPEPEADY 13
 ES +PEPEPE DY
 Sbjct: 57 ESADPEPEPETDY 69

tr Q68FX4 Hematopoietic cell specific Lyn substrate 1 (Predicted) 476 AA
 Q68FX4_RAT [Hcls1_predicted] [Rattus norvegicus (Rat)]
align

Score = 33.7 bits (72), Expect = 0.48
 Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
 EPEPEPE DY
 Sbjct: 369 EPEPEPEPDY 378

tr Q6T890 TonB2 [tonB2] [Actinobacillus pleuropneumoniae] 285
 Q6T890_ACTPL [Haemophilus
 pleuropneumoniae] AA
align

Score = 33.3 bits (71), Expect = 0.64
 Identities = 9/10 (90%), Positives = 10/10 (100%)

Query: 3 VEPEPEPEAD 12
 VEPEPEPEA+
 Sbjct: 73 VEPEPEPEAE 82

tr Q4R7C6 Testis cDNA, clone: QtsA-15617, similar to human 475
 Q4R7C6_MACFA hematopoietic AA
 cell-specific Lyn substrate 1 (HCLS1), mRNA, RefSeq:
 NM_005335.3 [Macaca fascicularis (Crab eating macaque)
 (Cynomolgus monkey)] align

Score = 33.3 bits (71), Expect = 0.64
 Identities = 11/16 (68%), Positives = 11/16 (68%), Gaps = 3/16 (18%)

Query: 1 ESV---EPEPEPEADY 13
 E V EPEPEPE DY
 Sbjct: 357 EPVYEAEPPEPENDY 372

sp P14317 Hematopoietic lineage cell specific protein 486
 HCLS1_HUMAN (Hematopoietic AA
 cell-specific LYN substrate 1) (LckBP1) (p75) [HCLS1] align
 [Homo sapiens (Human)]

Score = 32.9 bits (70), Expect = 0.86
 Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
 EPEPEPE DY
 Sbjct: 369 EPEPEPENDY 378

tr Q6IBK9 HCLS1 protein [HCLS1] [Homo sapiens (Human)] 486 AA
 Q6IBK9_HUMAN align

Score = 32.9 bits (70), Expect = 0.86
 Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
 EPEPEPE DY
 Sbjct: 369 EPEPEPENDY 378

tr Q53Y93 Hematopoietic cell-specific Lyn substrate 1 [Homo 486
 Q53Y93_HUMAN sapiens (Human)] AA align

Score = 32.9 bits (70), Expect = 0.86
 Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
 EPEPEPE DY
 Sbjct: 369 EPEPEPENDY 378

tr Q87MK6 Hypothetical protein VP2226 [VP2226] [Vibrio 370
 Q87MK6_VIBPA parahaemolyticus] AA align

Score = 32.5 bits (69), Expect = 1.1
 Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 2 SVEPEPEPE 10
 .SVEPEPEPE
 Sbjct: 43 SVEPEPEPE 51

tr Q9EN57 Zinc finger protein [Spodoptera litura multicapsid 497 AA

Q9EN57_NPVST nucleopolyhedrovirus (SpltMNPV)]

align

Score = 32.0 bits (68), Expect = 1.5
 Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 ESVEPEPEPE 10

ES EPEPEPE

Sbjct: 355 ESAEPEPEPE 364

tr Q91BL1 HOAR [Spodoptera litura multicapsid nucleopolyhedrovirus 731 AA
Q91BL1_NPVST (SpltMNPV)]

align

Score = 32.0 bits (68), Expect = 1.5
 Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 ESVEPEPEPE 10

ES EPEPEPE

Sbjct: 459 ESAEPEPEPE 468

tr Q8BGM6 Mus musculus 10 days neonate cerebellum cDNA, RIKEN 151
Q8BGM6_MOUSE full-length AA
 enriched library, clone:B930008A12 product:similar to align
 PP2CH (Mus musculus 0 day neonate eyeball cDNA, RIKEN
 full-length enriched library, clone:E130208E03
 product:similar to PP2CH) [Ppm1e] [Mus musculus
 (Mouse)]

Score = 32.0 bits (68), Expect = 1.5
 Identities = 10/12 (83%), Positives = 11/12 (91%), Gaps = 1/12 (8%)

Query: 1 ESVEPEPEPEAAD 12

ES EPEPEPEA+

Sbjct: 36 ES-EPEPEPEAE 46

tr Q80Z30 Calmodulin-dependent protein kinase phosphatase N [Ppm1e] 750
Q80Z30_RAT [Rattus AA
 norvegicus (Rat)] align

Score = 32.0 bits (68), Expect = 1.5
 Identities = 10/12 (83%), Positives = 11/12 (91%), Gaps = 1/12 (8%)

Query: 1 ESVEPEPEPEAAD 12.

ES EPEPEPEA+

Sbjct: 36 ES-EPEPEPEAE 46

tr Q5SX30 Protein phosphatase 1E (PP2C domain containing) [Ppm1e] 749
Q5SX30_MOUSE [Mus
musculus (Mouse)] AA
align

Score = 32.0 bits (68), Expect = 1.5
Identities = 10/12 (83%), Positives = 11/12 (91%), Gaps = 1/12 (8%)

Query: 1 ESVEPEPEPEAD 12
ES EPEPEPEA+
Sbjct: 36 ES-EPEPEPEAE 46

tr Q80VJ8 Hypothetical protein BC050196 [BC050196] [Mus musculus 578
Q80VJ8_MOUSE (Mouse)] AA
align

Score = 31.6 bits (67), Expect = 2.1
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 ESVEPEPEPE 10
E VEPEPEPE
Sbjct: 402 EEVEPEPEPE 411

tr Q6CE67 Similarity [YALI0B18172g] [Yarrowia lipolytica (Candida 1080 AA
Q6CE67_YARLI lipolytica)] AA
align

Score = 31.6 bits (67), Expect = 2.1
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 1 ESVEPEPEPE 10
E VEPEPEPE
Sbjct: 116 EEVEPEPEPE 125

tr Q9VT49 CG14168-PA [CG14168] [Drosophila melanogaster (Fruit 734
Q9VT49_DROME fly)] AA
align

Score = 31.2 bits (66), Expect = 2.8
Identities = 10/12 (83%), Positives = 10/12 (83%)

Query: 1 ESVEPEPEPEAD 12
E VEPEPEPE D
Sbjct: 348 EVVEPEPEPEKD 359

tr P91156 Hypothetical protein [C43E11.1] [Caenorhabditis elegans] 580 AA
P91156_CAEEL AA
align

Score = 31.2 bits (66), Expect = 2.8
Identities = 10/12 (83%), Positives = 10/12 (83%), Gaps = 2/12 (16%)

Query: 3 VEPE--PEPEAD 12
VEPE PEPEAD
Sbjct: 118 VEPEAEPEPEAD 129

tr Q5KGJ5 Hypothetical protein [CNE03390] [Cryptococcus neoformans 498 AA
Q5KGJ5_CRYNE (Filobasidiella neoformans)]
align

Score = 31.2 bits (66), Expect = 2.8
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
EPEPEPE +Y
Sbjct: 300 EPEPEPEPEY 309

tr Q55S44 Hypothetical protein [CNBE3380] [Cryptococcus neoformans 303
Q55S44_CRYNE var.
neoformans B-3501A]
align

Score = 31.2 bits (66), Expect = 2.8
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
EPEPEPE +Y
Sbjct: 111 EPEPEPEPEY 120

tr Q8I4T3 PFG377 protein [PFL2405c] [Plasmodium falciparum 3119
Q8I4T3_PLAF7 (isolate 3D7)]
align

Score = 30.8 bits (65), Expect = 3.7
Identities = 10/13 (76%), Positives = 11/13 (83%), Gaps = 1/13 (7%)

Query: 1 ESV-EPEPEPEAD 12
E V EPEPEPEA+
Sbjct: 123 EEVREPEPEPEAE 135

tr Q26022 Plasmodium falciparum sexual stage mRNA sequence. 754
Q26022_PLAFA (Fragment)
[Plasmodium falciparum]
align

Score = 30.8 bits (65), Expect = 3.7
Identities = 10/13 (76%), Positives = 11/13 (83%), Gaps = 1/13 (7%)

Query: 1 ESV-EPEPEPEAD 12
 E V EPEPEPEA+
Sbjct: 123 EEVREPEPEPEAE 135

tr Q25857 Pfg377 [Plasmodium falciparum] 3119 AA
 Q25857_PLAFA align

Score = 30.8 bits (65), Expect = 3.7
Identities = 10/13 (76%), Positives = 11/13 (83%), Gaps = 1/13 (7%)

Query: 1 ESV-EPEPEPEAD 12
 E V EPEPEPEA+
Sbjct: 123 EEVREPEPEPEAE 135

tr Q7S935 Predicted protein [NCU07949.1] [Neurospora crassa] 2826 AA
 Q7S935_NEUCR align

Score = 30.8 bits (65), Expect = 3.7
Identities = 10/13 (76%), Positives = 10/13 (76%), Gaps = 1/13 (7%)

Query: 1 ESV-EPEPEPEAD 12
 E V EPEPEPE D
Sbjct: 708 EPVAEPEPEPEPD 720

tr Q52FL1 Hypothetical protein [MG01625.4] [Magnaporthe grisea] 6586 AA
 Q52FL1_MAGGR 70-15 align

Score = 30.8 bits (65), Expect = 3.7
Identities = 10/11 (90%), Positives = 10/11 (90%), Gaps = 1/11 (9%)

Query: 1 ESVEPEPEPEA 11
 ESV PEPEPEA
Sbjct: 4949 ESV-PEPEPEA 4958

sp Q9D1X0 Nucleolar protein 3 [Nol3] [Mus musculus (Mouse)] 220 AA
 NOL3_MOUSE align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
 EPEPEPE D+
Sbjct: 202 EPEPEPEPDF 211

sp Q8XRH0 DNA translocase ftsK 1 [ftsK1] [Ralstonia solanacearum] 959
FTSK1_RALSO (Pseudomonas solanacearum) AA align

Score = 30.3 bits (64), Expect = 5.0
 Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
 EPEPEPEA+
 Sbjct: 334 EPEPEPEAE 342

sp Q9GLM6 Apolipoprotein E precursor (Apo-E) [APOE] [Hylobates lar] 317
APOE_HYLLA (Common gibbon) AA align

Score = 30.3 bits (64), Expect = 5.0
 Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 1 ESVEPEPEPE 10
 + VEPEPEPE
 Sbjct: 22 QAVEPEPEPE 31

tr Q8R2S3 Nucleolar protein 3 [No13] [Mus musculus (Mouse)] 220 AA
Q8R2S3_MOUSE align

Score = 30.3 bits (64), Expect = 5.0
 Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
 EPEPEPE D+
 Sbjct: 202 EPEPEPEPDF 211

tr Q8C550 Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230035L15 product:apoptosis repressor with CARD domain [No13] [Mus musculus (Mouse)] 220
Q8C550_MOUSE AA align

Score = 30.3 bits (64), Expect = 5.0
 Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
 EPEPEPE D+
 Sbjct: 202 EPEPEPEPDF 211

tr Q53YU5 Apoptosis repressor interacting with CARD (0 day neonate) 220

Q53YU5_MOUSE eyeball AA
 cDNA, RIKEN full-length enriched library,
 clone:E130314L04 product:apoptosis repressor with CARD
 domain) [Nol3] [Mus musculus (Mouse)] align

Score = 30.3 bits (64), Expect = 5.0
 Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 4 EPEPEPEADY 13
 EPEPEPE D+
 Sbjct: 202 EPEPEPEPDF 211

tr Q73XH7 Fas [fas] [Mycobacterium paratuberculosis] 3092 AA
 Q73XH7_MYCPA align

Score = 30.3 bits (64), Expect = 5.0
 Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
 +PEPEPEAD
 Sbjct: 1744 DPEPEPEAD 1752

tr Q478V8 Response regulator receiver:CheW-like protein:ATP- 1866
 Q478V8_9RHOO binding region, AA
 ATPase-like:Hpt [Daro_3895] [Dechloromonas aromatica align
 RCB]

Score = 30.3 bits (64), Expect = 5.0
 Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
 EPEPEPEA+
 Sbjct: 831 EPEPEPEAE 839

tr Q9EXU1 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
 Q9EXU1_KLEPN align

Score = 30.3 bits (64), Expect = 5.0
 Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 3 VEPEPEPEAD 12
 VEPEPEPE +
 Sbjct: 42 VEPEPEPETE 51

tr Q6XXM0 Fatty acid synthetase I [fas1] [Mycobacterium 3089

Q6XXM0_MYCSM smegmatis]

AA
align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
+PEPEPEAD
Sbjct: 1747 DPEPEPEAD 1755

tr Q5MBX2 TonB2 [tonB2] [Actinobacillus suis] 281 AA
Q5MBX2_ACTSU

align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 74 EPEPEPEAE 82

tr Q4QZC1 Periplasmic energy transducer (Fragment) [tonB] 138
Q4QZC1_KLEPN [Klebsiella pneumoniae]

AA
align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 3 VEPEPEPEAD 12
VEPEPEPE +
Sbjct: 21 VEPEPEPETE 30

tr Q9VAI5 CG15506-PB, isoform B [CG15506] [Drosophila melanogaster] 336
Q9VAI5_DROME (Fruit fly)]

AA
align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 321 EPEPEPEAE 329

tr Q9N411 Prion-like-(Q/n-rich)-domain-bearing protein protein 82 300
Q9N411_CAEEL [pqn-82]
[Caenorhabditis elegans]

AA
align

Score = 30.3 bits (64), Expect = 5.0

Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 2 SVEPEPEPEA 11

SVE EPEPEA

Sbjct: 244 SVEQEPEPEA 253

tr Q8MZB6 AT15667p [CG15506] [Drosophila melanogaster (Fruit fly)] 297 AA
Q8MZB6_DROME

align

Score = 30.3 bits (64), Expect = 5.0

Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12

EPEPEPEA+

Sbjct: 282 EPEPEPEAE 290

tr Q8IMK6 CG15506-PA, isoform A [CG15506] [Drosophila melanogaster 297
Q8IMK6_DROME (Fruit AA
fly)]

align

Score = 30.3 bits (64), Expect = 5.0

Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12

EPEPEPEA+

Sbjct: 282 EPEPEPEAE 290

tr Q4U8R9 Hypothetical protein [TA10045] [Theileria annulata] 599 AA
Q4U8R9_THEAN

align

Score = 30.3 bits (64), Expect = 5.0

Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12

EPEPEPEA+

Sbjct: 315 EPEPEPEAE 323

tr Q5AQG7 Hypothetical protein [AN9463.2] [Aspergillus nidulans 1737
Q5AQG7_EMENI FGSC A4]

AA

align

Score = 30.3 bits (64), Expect = 5.0

Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12

EPEPEPEA+
Sbjct: 448 EPEPEPEAE 456

tr Q5ARP0 Predicted protein [AN9040.2] [Aspergillus nidulans FGSC 179
Q5ARP0_EMENI A4]
align

Score = 30.3 bits (64), Expect = 5.0
Identities = 10/14 (71%), Positives = 10/14 (71%), Gaps = 4/14 (28%)

Query: 3 VEPEPE----PEAD 12
VEPEPE PEAD
Sbjct: 95 VEPEPEPEPAPPEAD 108

tr Q5ATE5 Hypothetical protein [AN8435.2] [Aspergillus nidulans 850
Q5ATE5_EMENI FGSC A4]
align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 661 EPEPEPEAE 669

tr Q527B1 Hypothetical protein [MG06645.4] [Magnaporthe grisea 70- 717
Q527B1_MAGGR 15]
align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 356 EPEPEPEAE 364

tr Q526E4 Hypothetical protein [MG06862.4] [Magnaporthe grisea 70- 919
Q526E4_MAGGR 15]
align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 466 EPEPEPEAE 474

tr Q4PFF2 Hypothetical protein [UM01161.1] [Ustilago maydis 521] 2649 AA
Q4PFF2_USTMA align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 9/9 (99%)

Query: 4 EPEPEPEAD 12
EPEPEPEA+
Sbjct: 2312 EPEPEPEAE 2320

tr Q4IFF5 Hypothetical protein [FG04053.1] [Gibberella zeae PH-1] 807 AA
Q4IFF5_GIBZE align

Score = 30.3 bits (64), Expect = 5.0
Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 5 PEPEPEADY 13
PEPEPE DY
Sbjct: 236 PEPEPEPDY 244

sp P26185 TonB protein [tonB] [Serratia marcescens] 247 AA
TONB_SERMA align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 75 VEPEPEPE 82

sp P25945 TonB protein [tonB] [Salmonella typhimurium] 242 AA
TONB_SALTY align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 69 VEPEPEPE 76

sp P45610 TonB protein [tonB] [Klebsiella pneumoniae] 243 AA
TONB_KLEPN

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 68 VEPEPEPE 75

sp P46383 TonB protein [tonB] [Enterobacter aerogenes (Aerobacter aerogenes)] 243 AA

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 69 VEPEPEPE 76

sp P02929 TonB protein [tonB] [Escherichia coli] 239 AA

TONB_ECOLI

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 69 VEPEPEPE 76

sp Q62881 Nucleolar protein 3 [Nol3] [Rattus norvegicus (Rat)] 221 AA

NOL3_RAT

align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 179 VEPEPEPE 186

sp P97855 Ras-GTPase-activating protein binding protein 1 (GAP SH3-
G3BP_MOUSE domain 465
binding protein 1) (G3BP-1) (DNA helicase VIII)
(HDH-VIII) [G3bp] [Mus musculus (Mouse)]

AA

align

Score = 29.9 bits (63), Expect = 6.7

Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10

VEPEPEPE

Sbjct: 191 VEPEPEPE 198

tr Q4SUQ6 Chromosome undetermined SCAF13844, whole genome shotgun 129
Q4SUQ6_TETNG sequence AA
[GSTENG00012352001] [Tetraodon nigroviridis (Green align
puffer)]

Score = 29.9 bits (63), Expect = 6.7

Identities = 8/9 (88%), Positives = 8/9 (88%)

Query: 4 EPEPEPEAD 12

EPEPEPE D

Sbjct: 90 EPEPEPETD 98

tr Q62882 Hypothetical protein [Rattus norvegicus (Rat)] 139 AA
Q62882_RAT align

Score = 29.9 bits (63), Expect = 6.7

Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10

VEPEPEPE

Sbjct: 97 VEPEPEPE 104

tr Q5NCU1 Ras-GTPase-activating protein SH3-domain binding protein 465 AA
Q5NCU1_MOUSE [RP23-336J1.4] [Mus musculus (Mouse)] align

Score = 29.9 bits (63), Expect = 6.7

Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10

VEPEPEPE

Sbjct: 191 VEPEPEPE 198

tr Q571F9 MKIAA4115 protein (Fragment) [G3bp] [Mus musculus 505
Q571F9_MOUSE (Mouse)] AA align

Score = 29.9 bits (63), Expect = 6.7

Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 231 VEPEPEPEPE 238

tr Q57P65 SsrAB activated gene [srfA] [Salmonella choleraesuis] 441 AA
Q57P65_SALCH align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 169 VEPEPEPEPE 176

tr Q57NS2 Energy transducer; uptake of iron, cyanocobalimin; 281
Q57NS2_SALCH sensitivity to AA
phages, colicins [tonB] [Salmonella choleraesuis] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 110 VEPEPEPEPE 117

tr Q9S3M6 TonB protein (Siderophore-mediated iron transport 266
Q9S3M6_BORPE protein) [tonB] AA
[Bordetella pertussis] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 101 VEPEPEPEPE 108

tr Q8Z7E4 TonB protein [tonB] [Salmonella typhi] 242 AA
Q8Z7E4_SALTI align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 69 VEPEPEPEPE 76

tr Q8XCC2 Energy transducer; uptake of iron, cyanocobalimin; 239
Q8XCC2_ECO57 sensitivity to AA
phages, colicins [tonB] [Escherichia coli O157:H7] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 69 VEPEPEPE 76

tr Q8FHW5 TonB protein [tonB] [Escherichia coli O6] 255 AA
Q8FHW5_ECOL6 align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 86 VEPEPEPE 93

tr Q885B3 Major facilitator family transporter [PSPTO1922] 465
Q885B3_PSESM [Pseudomonas AA
syringae pv. tomato] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 422 VEPEPEPE 429

tr Q884X6 Flagellar assembly protein Flih, putative [PSPTO1960] 272 AA
Q884X6_PSESM [Pseudomonas syringae pv. tomato] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE
Sbjct: 33 VEPEPEPE 40

tr Q83RM7 Membrane protein, energy transducer [tonB] [Shigella 242
Q83RM7_SHIFL flexneri] AA
align

Score = 29.9 bits (63), Expect = 6.7
 Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
 Sbjct: 72 VEPEPEPE 79

tr Q7WKX3 Siderophore-mediated iron transport protein [tonB] 268
Q7WKX3_BORBR [Bordetella AA
 bronchiseptica (Alcaligenes bronchisepticus)] align

Score = 29.9 bits (63), Expect = 6.7
 Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
 Sbjct: 103 VEPEPEPE 110

tr Q7W7I4 Siderophore-mediated iron transport protein [tonB] 278
Q7W7I4_BORPA [Bordetella AA
 parapertussis] align

Score = 29.9 bits (63), Expect = 6.7
 Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
 Sbjct: 113 VEPEPEPE 120

Score = 29.9 bits (63), Expect = 6.7
 Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE
 Sbjct: 103 VEPEPEPE 110

tr Q5PHV4 Putative virulence effector protein [srfA] [Salmonella 399
Q5PHV4_SALPA paratyphi-a] AA
align

Score = 29.9 bits (63), Expect = 6.7
 Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
 VEPEPEPE

Sbjct: 127 VEPEPEPE 134

tr Q5PCS7 TonB protein [tonB] [Salmonella paratyphi-a] 242 AA
Q5PCS7_SALPA align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE

Sbjct: 69 VEPEPEPE 76

tr Q5Nzs1 Translation initiation factor IF-2 [infB] [Azoarcus sp. 945
Q5Nzs1_AZOSE (strain AA
Ebn1)] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE

Sbjct: 159 VEPEPEPE 166

tr Q48GE4 Flagellar assembly protein Flh [fliH] [Pseudomonas 274
Q48GE4_PSESH syringae pv. AA
phaseolicola 1448A] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE

Sbjct: 33 VEPEPEPE 40

tr Q9ZG18 TonB [tonB] [Bordetella bronchiseptica (Alcaligenes 268 AA
Q9ZG18_BORBR bronchisepticus)] align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPE 10
VEPEPEPE

Sbjct: 103 VEPEPEPE 110

tr Q9S3Z9 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9S3Z9_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 42 VEPEPEPEPE 49

tr Q9S3Z7 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9S3Z7_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 42 VEPEPEPEPE 49

tr Q9S3Z6 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9S3Z6_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 42 VEPEPEPEPE 49

tr Q9R440 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9R440_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 42 VEPEPEPEPE 49

tr Q9R427 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9R427_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 42 VEPEPEPEPE 49

tr Q9R426 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9R426_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 42 VEPEPEPEPE 49

tr Q9EXU0 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9EXU0_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 42 VEPEPEPEPE 49

tr Q9EXT9 TonB (Fragment) [tonB] [Klebsiella pneumoniae] 180 AA
Q9EXT9_KLEPN
align

Score = 29.9 bits (63), Expect = 6.7
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 3 VEPEPEPEPE 10
VEPEPEPEPE
Sbjct: 42 VEPEPEPEPE 49

Database: EXPASY/UniProtKB
Posted date: Sep 12, 2005 12:34 PM
Number of letters in database: 758,486,757
Number of sequences in database: 2,312,053

Lambda K H
0.319 0.283 1.59

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
length of query: 13
length of database: 758,486,757
effective HSP length: 4
effective length of query: 9
effective length of database: 749,238,545
effective search space: 6743146905
effective search space used: 6743146905
T: 16
A: 40
X1: 16 (7.4 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 43 (21.6 bits)
S2: 62 (29.5 bits)

Wallclock time: 3 seconds

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entry Q53H67

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[\[References\]](#)
[\[Comments\]](#)
[\[Cross-references\]](#)
[\[Keywords\]](#)

[\[Features\]](#)
[\[Sequence\]](#)
[\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	Q53H67_HUMAN
Primary accession number	Q53H67
Secondary accession numbers	None
Entered in TrEMBL in	Release 31, September 2005
Sequence was last modified in	Release 31, September 2005
Annotations were last modified in	Release 31, September 2005

Name and origin of the protein

Protein name	Left-right determination, factor B preproprotein variant [Fragment]
Synonyms	None
Gene name	Name: LEFTY1
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

References

[1] NUCLEOTIDE SEQUENCE.

TISSUE=Colon;
 Maruyama K., Sugano S.;
 "Oligo-capping : a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides.";
 Gene 138:171-174(1994).

[2] NUCLEOTIDE SEQUENCE.

TISSUE=Colon;
 Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
 "Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library.";
 Gene 200:149-156(1997).

[3] NUCLEOTIDE SEQUENCE.

TISSUE=Colon;
 Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
 Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.

Comments

- **SIMILARITY:** Belongs to the TGF-beta family.

Cross-references

EMBL AK222714; BAD96434.1; -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

Ensembl	ENSG00000143787; Homo sapiens. [Contig view]
HGNC	HGNC:6552; LEFTY1.
CleanEx	HGNC:6552; LEFTY1.
GeneCards	LEFTY1.
GeneLynx	LEFTY1; Homo sapiens.
GenAtlas	LEFTY1.
	GO:0008083; Molecular function: growth factor activity (<i>inferred from electronic annotation</i>).
GO	GO:0005160; Molecular function: transforming growth factor beta receptor binding (<i>inferred from electronic annotation</i>).
	GO:0016049; Biological process: cell growth (<i>inferred from electronic annotation</i>).
	QuickGo view.
	IPR001839; TGFb.
InterPro	IPR003942; TGFb4.
	IPR001111; TGFb_N.
	Graphical view of domain structure.
Pfam	PF00019; TGF_beta; 1.
	PF00688; TGFb_propeptide; 1.
	Pfam graphical view of domain structure.
PRINTS	PR01427; TGFBETA4.
ProDom	PD000357; TGFb; 1. [Domain structure / List of seq. sharing at least 1 domain]
SMART	SM00204; TGFB; 1.
PROSITE	PS00250; TGF_BETA_1; 1.
HOVERGEN	[Family / Alignment / Tree]
ProtoMap	Q53H67.
PRESAGE	Q53H67.
ModBase	Q53H67.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords**Growth factor.****Features**

Feature table viewer

Key	From	To	Length	Description
NON_TER	1	1		

Sequence information

Length: 366 AA [This is the length of the partial sequence] Molecular weight: 40826 Da [This is the MW of the partial sequence]

CRC64: A5AA26DE37658075 [This is a checksum on the sequence]

102030405060

MQPLWLCWAL WVLPLASPGA ALTGEQLLGS LLRQLQLKEV PTLDRADMEE LVIPTHVRAQ

70 80 90 100 110 120
YVALLQRSHG DRSRGKRF SQ SFREVAGRFL ASEASTHLLV FGMEQRLPPN SELVQAVRL

130 140 150 160 170 180
FQEVPVKAAL HRHGRLSPRS AQARVTVEWL RVRDDGSNRT SLIDSRLVSV HESGWKAFDV

190 200 210 220 230 240
TEAVNFWQQL SRPRQPPLLQ VSVQREHLGP LASGAHKLVR FASQGAPAGL GEPQLELHTL

250 260 270 280 290 300
DLG DYGAQGD CDPEAPMTEG TRCCRQEMYI DLQGMKWAEN WVLEPPGFLA YECVGTCRQP

310 320 330 340 350 360
PEALAFKWP F LGPRQCIASE TDSLPMIVSI KEGGRTRPQV VSLPNMRVQK CSCASDGALV

PRRLQP

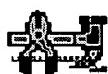
Q53H67 in FASTA format

View entry in original UniProtKB/TrEMBL format

View entry in raw text format (no links)

Request for annotation of this UniProtKB/TrEMBL entry

BLAST BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



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NPS@ NPSA Sequence analysis tools

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==SPRINT==> PRINTS View

selected as

© PR01427

Identifier	TGFBETA4 [View Relations] [View Alignment]
Accession	PR01427
No. of Motifs	14
Creation Date	01-NOV-2000
Title	Transforming growth factor beta 4 precursor signature
Database References	PRINTS; PR01423 TGFBETA MIM; 601877
Literature References	<p>1. KOTHAPALLI, R., BUYUKSAL, I., WU, S.-Q., CHEGINI, N. AND TABIBZADEH Detection of eba, a novel human gene of the transforming growth factor beta superfamily association of gene expression with endometrial bleeding. <i>J.CLIN.INVEST.</i> 99 2342-2350 (1997).</p> <p>2. MENO, C., SAIJOH, Y., FUJII, H., IKEDA, M., YOKOYAMA, T., YOKOYAMA, TOYODA, Y. AND HAMADA, H. Left-right asymmetric expression of the TGF beta-family member lefty mouse embryos. <i>NATURE</i> 381 151-155 (1996).</p>
Documentation	<p>Abnormal endometrial bleeding is a common manifestation of gynaecological diseases. A human gene, termed endometrial bleeding associated factor which is expressed strongly in endometrium, has been shown to be associated with abnormal endometrial bleeding [1]. The predicted protein product eba shares similarity with members of TGF-beta superfamily. Thus eba is a novel member of the TGF-beta superfamily and an endometrial tissue factor whose expression is associated with normal menstrual and abnormal endometrial bleeding [1].</p> <p>Examples of lateral asymmetry are often found in vertebrates (e.g., the heart being on the left side), but the molecular mechanisms governing establishment of left-right (L-R) handedness are unknown [2]. It is thought that the gene lefty, a member of the transforming growth factor beta family, may encode a morphogen for L-R determination [2]. Lefty protein which contains the cysteine-knot motif characteristic of this superfamily.</p>

is expressed in the left half of gastrulating mouse embryos. This asymmetrical expression is transient and occurs just before the first sign of late asymmetry appears [2]. Thus lefty may be involved in establishing L-R asymmetry in the organ systems of mammals [2].

TGFBETA4 is a 14-element fingerprint that provides a signature for the transforming growth factor beta 4 precursor proteins. The fingerprint derived from an initial alignment of 2 sequences: the motifs were drawn from conserved regions spanning virtually the full alignment length, focusing those sections that characterise TGF-beta 4 proteins but distinguishing from the rest of the TGF-beta superfamily. Two iterations on SPTR39_1 were required to reach convergence, at which point a true set comprising 4 sequences was identified. Several partial matches were also found (Q9W6I7, Q9PW55, Q9W6I6), all antivin or Lefty proteins that match 2-4

Summary Information

4 codes involving 14 elements
 0 codes involving 13 elements
 0 codes involving 12 elements
 0 codes involving 11 elements
 0 codes involving 10 elements
 0 codes involving 9 elements
 0 codes involving 8 elements
 0 codes involving 7 elements
 0 codes involving 6 elements
 0 codes involving 5 elements
 1 codes involving 4 elements
 1 codes involving 3 elements
 2 codes involving 2 elements

Composite Feature Index

14	4	4	4	4	4	4	4	4	4	4	4	4	4	4
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	1	0	0	0	0	0	1	0	0	1	1	0	0
3	0	0	0	0	1	0	0	1	0	0	1	0	0	0
2	0	0	2	0	0	0	0	2	0	0	0	0	0	0
	1	2	3	4	5	6	7	8	9	10	11	12	13	14

True Positives	<u>075610</u>	<u>075611</u>	<u>TGF4_HUMAN</u>	<u>TGF4_MOUSE</u>	
True Positive Partials	Codes involving 4 elements <u>Q9PVN4</u>				
	Codes involving 3 elements <u>Q9W6I7</u>				
	Codes involving 2 elements <u>Q9PW55</u> <u>Q9W6I6</u>				
Sequence Titles	<u>075610</u>	SIGNALING MOLECULE LEFTY-B - Homo sapiens (Human).			
	<u>075611</u>	SIGNALING MOLECULE LEFTY-A - Homo sapiens (Human).			
	<u>TGF4_HUMAN</u>	TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4)			
	<u>TGF4_MOUSE</u>	TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4)			
	<u>Q9PVN4</u>	LEFTY - Gallus gallus (Chicken).			
	<u>Q9W6I7</u>	SIGNALING MOLECULE LEFTY2 - Brachydanio rerio (Zebrafish)			
	<u>Q9PW55</u>	ANTIVIN - Brachydanio rerio (Zebrafish) (Zebra danio).			
	<u>Q9W6I6</u>	SIGNALING MOLECULE LEFTY1 - Brachydanio rerio (Zebrafish)			
Scan History	SPTR39_14f 2 50 NSINGLE				
Initial Motifs	Motif 1 width=23				
	Element	Seqn Id	St	Int	Rpt
	LWLCWALWVLPLAGPGAAALTEEQ	TGF4_HUMAN	4	4	-
	LWLCWALWALSILVSLREALTGEQ	TGF4_MOUSE	4	4	-
	Motif 2 width=22				
	Element	Seqn Id	St	Int	Rpt
	QILGSLLQQQLQLDQPPVLDKAD	TGF4_MOUSE	26	-1	-
	QLLASLLRQLQLSEVPVLDRAD	TGF4_HUMAN	26	-1	-
	Motif 3 width=17				
	Element	Seqn Id	St	Int	Rpt
	EGMVIPSHVRTQYVALL	TGF4_MOUSE	49	1	-
	EKLVIPAHVRAQYVVLL	TGF4_HUMAN	49	1	-
	Motif 4 width=19				
	Element	Seqn Id	St	Int	Rpt
	RSRGKRFSQNLREVAGRFL	TGF4_MOUSE	72	6	-
	RSRGKRFSQSFRREVAGRFL	TGF4_HUMAN	71	5	-
	Motif 5 width=16				
	Element	Seqn Id	St	Int	Rpt
	HLLVFGMEQRLLPPNSE	TGF4_MOUSE	97	6	-
	HLLVFGMEQRLLPPNSE	TGF4_HUMAN	96	6	-
	Motif 6 width=21				
	Element	Seqn Id	St	Int	Rpt
	ELVQAVLRLFQEPVPQGALHR	TGF4_HUMAN	111	-1	-
	ELVQAVLRLFQEPVPRTALRR	TGF4_MOUSE	112	-1	-
	Motif 7 width=19				
	Element	Seqn Id	St	Int	Rpt
	RQKRLSPHSARARVTIEWL	TGF4_MOUSE	132	-1	-
	RHGRLSPAAPKARVTVEWL	TGF4_HUMAN	131	-1	-

Motif 8 width=22		Seqn Id	St	Int	Rpt
Element		TGF4_MOUSE	153	2	-
RDDGSNRTALIDSRLVSIHESG		TGF4_HUMAN	151	1	-
Motif 9 width=24		Seqn Id	St	Int	Rpt
Element		TGF4_MOUSE	187	12	-
WQQLSRPRQPLLLQVSVQREHLGP		TGF4_HUMAN	185	12	-
Motif 10 width=16		Seqn Id	St	Int	Rpt
Element		TGF4_MOUSE	216	5	-
HKLVRFAAQGTPDGKG		TGF4_HUMAN	214	5	-
HKLVRFASQGAPAGLG					
Motif 11 width=26		Seqn Id	St	Int	Rpt
Element		TGF4_MOUSE	236	4	-
QLELHTLDLKDYGAQGNCDPEAPVTE		TGF4_HUMAN	232	2	-
QLELHTLDLRDYGAQGDCDPEAPMTE					
Motif 12 width=22		Seqn Id	St	Int	Rpt
Element		TGF4_MOUSE	267	5	-
RQEMYLDLQGMKWAENWILEPP		TGF4_HUMAN	263	5	-
RQEMYIDLQGMKWAKNWVLEPP					
Motif 13 width=21		Seqn Id	St	Int	Rpt
Element		TGF4_MOUSE	301	12	-
QLPESLTSRWPFGLGPRQCVAS		TGF4_HUMAN	297	12	-
QPPEALAFNWPFLGPRQCIAS					
Motif 14 width=20		Seqn Id	St	Int	Rpt
Element		TGF4_MOUSE	327	5	-
PMIVSVKEGGTRPQVVSLP		TGF4_HUMAN	323	5	-
PMIVSIKEGGTRPQVVSLP					
Final Motifs					
Motif 1 width=23		Seqn Id	St	Int	Rpt
Element		TGF4_HUMAN	4	4	-
LWLCWALWVLPLAGPGAALTEEQ		075610	4	4	-
LWLCWALWVLPLASPGAAALTGEQ		TGF4_MOUSE	4	4	-
LWLCWALWALSLVSLREALTGEQ		075611	4	4	-
LWLCWALWVLPLAGPGAALTEEQ					
Motif 2 width=22		Seqn Id	St	Int	Rpt
Element		TGF4_MOUSE	26	-1	-
QILGSLLQQQLQLDQPPPVLKDAD		TGF4_HUMAN	26	-1	-
QLLASLLRQLQLSEVPVLDRAD		075610	26	-1	-
QLLGSSLRQLQLKEVPTLDRAD		075611	26	-1	-
QLLGSSLRQLQLSEVPVLDRAD					
Motif 3 width=17		Seqn Id	St	Int	Rpt
Element		TGF4_MOUSE	49	1	-
EGMVIPSHVRTQYVALL		TGF4_HUMAN	49	1	-
EKLVIPAHVRAQYVVLL		075610	49	1	-
EELVIPTHVRAQYVALL		075611	49	1	-
EKLVIPAHVRAQYVVLL					
Motif 4 width=19		Seqn Id	St	Int	Rpt
Element					

RSRGKRFSQLREVAGRFL	<u>TGF4 MOUSE</u>	72	6	-
RSRGKRFSQLREVAGRFL	<u>TGF4 HUMAN</u>	71	5	-
RSRGKRFSQLREVAGRFL	<u>075610</u>	72	6	-
RSRGKRFSQLREVAGRFL	<u>075611</u>	72	6	-
Motif 5 width=16				
Element	Seqn Id	St	Int	Rpt
HLLVFGMEQRLLPPNSE	<u>TGF4 MOUSE</u>	97	6	-
HLLVFGMEQRLLPPNSE	<u>TGF4 HUMAN</u>	96	6	-
HLLVFGMEQRLLPPNSE	<u>075611</u>	97	6	-
HLLVFGMEQRLLPPNSE	<u>075610</u>	97	6	-
Motif 6 width=21				
Element	Seqn Id	St	Int	Rpt
ELVQAVLRLFQEVPVKAALHR	<u>075611</u>	112	-1	-
ELVQAVLRLFQEVPVPGALHR	<u>TGF4 HUMAN</u>	111	-1	-
ELVQAVLRLFQEVPVKAALHR	<u>075610</u>	112	-1	-
ELVQAVLRLFQEVPVRTALRR	<u>TGF4 MOUSE</u>	112	-1	-
Motif 7 width=19				
Element	Seqn Id	St	Int	Rpt
RQKRLSPHSARARVTIEWL	<u>TGF4 MOUSE</u>	132	-1	-
RHGRLSPAAPKARVTVEWL	<u>TGF4 HUMAN</u>	131	-1	-
RHGRLSPRSAQARVTVEWL	<u>075611</u>	132	-1	-
RHGRLSPRSARARVTVEWL	<u>075610</u>	132	-1	-
Motif 8 width=22				
Element	Seqn Id	St	Int	Rpt
RDDGSNRTALIDSRLVSIHESG	<u>TGF4 MOUSE</u>	153	2	-
RDDGSNRTSLIDSRLVSVHESG	<u>TGF4 HUMAN</u>	151	1	-
RDDGSNRTSLIDSRLVSVHESG	<u>075610</u>	153	2	-
RDDGSNRTSLIDSRLVSVHESG	<u>075611</u>	153	2	-
Motif 9 width=24				
Element	Seqn Id	St	Int	Rpt
WQQLSRPRQPLLLQVSVQREHLGP	<u>075610</u>	187	12	-
WQQLSRPRQPLLLQVSVQREHLGP	<u>075611</u>	187	12	-
WQQLSRPRQPLLLQVSVQREHLGP	<u>TGF4 MOUSE</u>	187	12	-
WQQLSRPPEPPLLQVSVQREHLGP	<u>TGF4 HUMAN</u>	185	12	-
Motif 10 width=16				
Element	Seqn Id	St	Int	Rpt
HKLVRFASQGAPAGLG	<u>075610</u>	216	5	-
HKLVRFASQGAPAGLG	<u>075611</u>	216	5	-
HKLVRFAAQGTPDGKG	<u>TGF4 MOUSE</u>	216	5	-
HKLVRFASQGAPAGLG	<u>TGF4 HUMAN</u>	214	5	-
Motif 11 width=26				
Element	Seqn Id	St	Int	Rpt
QLELHTLDLRDYGAQGDCDPEAPMTE	<u>075611</u>	234	2	-
QLELHTLDLGDYGAQGDCDPEAPMTE	<u>075610</u>	234	2	-
QLELHTLDLKDYGAQGNCDPEAPVTE	<u>TGF4 MOUSE</u>	236	4	-
QLELHTLDLRDYGAQGDCDPEAPMTE	<u>TGF4 HUMAN</u>	232	2	-
Motif 12 width=22				
Element	Seqn Id	St	Int	Rpt
RQEMYLDLQGMKWAENWILEPP	<u>TGF4 MOUSE</u>	267	5	-
RQEMYIDLQGMKWAKNWVLEPP	<u>TGF4 HUMAN</u>	263	5	-
RQEMYIDLQGMKWAENWVLEPP	<u>075610</u>	265	5	-

RQEMYIDLQGMKWAKNWVLEPP	<u>075611</u>	265	5	-
Motif 13 width=21				
Element	Seqn Id	St	Int	Rpt
QLPESLTSRWPFLGPRQCVAS	<u>TGF4 MOUSE</u>	301	12	-
QPPEALAFNWPFLGPRQCIAS	<u>TGF4 HUMAN</u>	297	12	-
QPPEALAFKWPFLGPRQCIAS	<u>075610</u>	299	12	-
QPPEALAFNWPFLGPRQCIAS	<u>075611</u>	299	12	-
Motif 14 width=20				
Element	Seqn Id	St	Int	Rpt
PMIVSVKEGGRTTRPQVVSLP	<u>TGF4 MOUSE</u>	327	5	-
PMIVSIKEGGRTTRPQVVSLP	<u>TGF4 HUMAN</u>	323	5	-
PMIVSIKEGGRTTRPQVVSLP	<u>075610</u>	325	5	-
PMIVSIKEGGRTTRPQVVSLP	<u>075611</u>	325	5	-

(data stored in EXT_LINK zone)

Hoverprot: TGFB4_MOUSE

ID TGFB4_MOUSE STANDARD; PRT; 368 AA.
AC Q64280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Transforming growth factor beta 4 precursor (TGF-beta 4) (Lefty protein) (Lefty-1 protein) (STRA3 protein).
GN Name=Ebaf; Synonyms=Lefty, Lefty1, Stra3, Tgfb4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96202359; PubMed=8610011; DOI=10.1038/381151a0;
RA Meno C., Saijoh Y., Fujii H., Ikeda M., Yokoyama T., Yokoyama M.,
RA Toyoda Y., Hamada H.;
RT "Left-right asymmetric expression of the TGF beta-family member lefty
in mouse embryos.";
RL Nature 381:151-155(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Bouillet P.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98156497; PubMed=9496783;
RA Oulad-Abdelghani M., Chazaud C., Bouillet P., Mattei M.-G., Dolle P.,
RA Chambon P.;
RT "Stra3/lefty, a retinoic acid-inducible novel member of the
transforming growth factor-beta superfamily.";
RL Int. J. Dev. Biol. 42:23-32(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE RNA].
RC TISSUE=Embryonic stem cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]

RP FUNCTION.

RX MEDLINE=98372436; PubMed=9708731; DOI=10.1016/S0092-8674(00)81472-5;

RA Meno C., Shimono A., Saijoh Y., Yashiro K., Mochida K., Ohishi S.,

RA Noji S., Kondoh H., Hamada H.;

RT "Lefty-1 is required for left-right determination as a regulator of
 RT lefty-2 and nodal.";

RL Cell 94:287-297 (1998).

CC --!- FUNCTION: Required for left-right axis determination as a
 CC regulator of LEFTY2 and NODAL.

CC --!- SUBCELLULAR LOCATION: Secreted.

CC --!- DEVELOPMENTAL STAGE: By E8.0, expressed exclusively on the left
 CC side of developing embryos with expression predominantly in the
 CC prospective floor plate (PFP). Weak expression in the lateral-
 CC plate mesoderm (LPM).CC --!- PTM: The processing of the protein may also occur at the second R-
 CC X-X-R site located at AA 132-135. Processing appears to be
 CC regulated in a cell-type specific manner.

CC --!- SIMILARITY: Belongs to the TGF-beta family.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.CC -----
 CC --!- GENE_FAMILY: HBG074429 [FAMILY / ALN / TREE]
 DR EMBL; D83921; BAA12121.1; -; mRNA.
 DR EMBL; Z73151; CAA97497.1; -; mRNA.
 DR EMBL; AJ000082; CAA03909.1; -; mRNA.
 DR EMBL; AJ000083; CAA03910.1; -; Genomic_DNA.
 DR EMBL; BC050221; AAH50221.1; -; mRNA.
 DR PIR; S67507; S67507.
 DR HSSP; P10600; 1TGJ.
 DR Ensembl; ENSMUSG00000038793; Mus musculus.
 DR MGI; MGI:107405; Ebaf.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF_beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR01427; TGFBETA4.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR PRODOM; Q64280.
 DR SWISS-2DPAGE; Q64280.

KW Cytokine; Developmental protein; Glycoprotein; Growth factor; Signal.

FT DOMAIN 16 74 PRODOM:2002.1:PD037776 11

FT DOMAIN 75 241 PRODOM:2002.1:PD583730 4

FT DOMAIN 242 362 PRODOM:2002.1:PD328043 10

FT SIGNAL 1 21 Potential.

FT PROPEP 22 76 Or 135 (Potential).

FT CHAIN 77 368 Transforming growth factor beta 4.

FT CARBOHYD 158 158 N-linked (GlcNAc...) (Potential).

FT DISULFID 253 266 By similarity.

FT DISULFID 265 318 By similarity.
FT DISULFID 295 353 By similarity.
FT DISULFID 299 355 By similarity.
SQ SEQUENCE 368 AA; 41498 MW; 821DAE663C546B5F CRC64;
MPFLWLCWAL WALSLVSLRE ALTGEQILGS LLQQLQLDQP PVLDKADVEG MVIPISHVRTQ
YVALLQHSHA SRSGRKFSQ NLREVAGRFL VSETSTHLLV FGMEQRLLPPN SELVQAVLRL
FQEPPVPTAL RRQKRLSPHS ARARVTIEWL RFRDDGSNRT ALIDSRLVSI HESGWKAFDV
TEAVNFWQQL SRPRQPLLLQ VSVQREHLGP GTWSSHKLVR FAAQGTPDGK GQGEPEQLELH
TLDLKDYGAQ GNCDPEAPVT EGTRCCRQEM YLDLQGMKWA ENWILEPPGF LTYECVGSC
QLPESLTCSRW PFLGPRQCVA SEMTSLPMIV SVKEGGRTRP QVVSLPNMRV QTCSCASDGA
LIPRRLQP

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